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     Pred. No. is the number of results predicted by chance to h score greater than or equal to the score of the result bein and is derived by analysis of the total score distribution.
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                    Bovine prion prote
Ovine prion protei
Human prion protei
Prion protein regi
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Prion mimetic pept
Octa-peptide motif
Prion protein, PrP
Prion protein, PrP
                                                                                                                                                                                                                                                                                                    Description
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234	7234	AAB72347	AAB72346	AAB72345	AAB72344	AAB72341	AAB72340	AAB72339	AAB72338	AAB82112	AAG65853	AAY81485	AAB06272	AAB15035	AAW85901	AAY07994	AAW69660	AAR86715	AAB72369	AAB72352	AAB72342	AAW93571	AAW70261	AAB07328	AAB07317	AAB30802	AAB30801	AAE15601	AAB82110	~	ω	AAB07318	073	AAW70280
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ALIGNMENTS

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RESULT 1
AAU11824
Prion protein; Prp; ligand; octapeptide motif; scrapie; prion-associated disease; Creutzfeldt-Jakob disease; Gerstmann-Straussler-Scheinker disease; fatal familial insomnia; feline spongiform encephalopathy; bovine spongiform encephalopathy; transmissible mink encephalopathy; exotic ungulate encephalopathy;
                                                                                           05-APR-2001;
        WPI; 2002-061944/08
                             Hammond DJ, Wiltshire VR,
                                                                       05-APR-2000;
                                                                                                                  18-OCT-2001.
                                                                                                                                     WO200177687-A2
                                                                                                                                                           Mammalia
                                                                                                                                                                               chronic wasting disease.
                                                                                                                                                                                                                                                       Prion protein, PrP, octapeptide motif.
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                                                                                                                                                                                                                                                                                                   AAU11824;
                                                                                                                                                                                                                                                                                                                      AAU11824 standard; peptide; 8 AA.
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                                                  TECHNOLOGIES INC.
                                                                       2000US-0543188
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Matches
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  Example;
                                                                            Inactivating transmissible spongiform encephalopathy (TSE) agent as Creutzfeldt-Jacob disease, scrapie, kuru or Gerstmann-Straussler-Scheinker syndrome involves exposing agent t
                                                                                                                                                                                              WPI;
                                                                                                                                                                                                                                                    Raven NDH
                                                                                                                                                                                                                                                                                                          (MICR-)
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26-FEB-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transmissible spongiform encephalopathy; prion protein; sterilisation; immunisation; Creutzfeldt Jacob disease; kuru; fatal familial insomnia; Gerstmann-Straussler-Scheinker syndrome; chronic wasting disease; bovine spongiform encephalopathy; feline spongiform encephalopathy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Prion mimetic
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                                                        thermostable
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transmissible mink
  Page
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larity 100.0%;
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2001GB-0004696.
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                                                                                                                                                                                                                                                                                                          AUTHORITY
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RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CC The present invention describes a method (M1) for inactivating a CC transmissible spongiform encephalopathy (TSE) agent comprising exposing CC the TSE agent to a thermostable proteolytic enzyme. Also described: CC (1) a composition (I) for inactivating a TSE agent, comprising a CC prion dimer which does not bind to a prion monomer; and (3) a purified CC prion dimer which does not bind to a prion monomer; and (3) a purified CC prion dimer (M1) is useful for inactivating a TSE agent kuru, fatal CC familial insomnia, Gerstmann-Straussler-Scheinker syndrome, bovine CC spongiform encephalopathy, scrapte, feline spongiform encephalopathy, (I) is chronic wasting disease or transmissible mink encephalopathy. (I) is CC useful for sterilising material contaminated with the TSE agent. A prion CC dimer is useful for examining a sample infected with or suspected to be infected by a prion protein, and for detecting prion infectivity, by CC detecting a prion dimer in the sample. A prion dimer is useful for cramining an animal with a prion dimer, obtaining its extract which contains (II), and isolating (II) from the extract. The method comprises obtaining an animal with a prion dimer, obtaining its capacity of the useful for inactivating TSE agents in potentially contaminated clinical waste and culled animal material. (M1) is useful for even walls of rooms. The present sequence represents a prion mimetic correspondence which is used in an example from the preparation in the correspondence which is useful for an example from the present and the prion dimer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                             Diagnosis of prion diseases, by treatment with proteinase detecting retention of octapeptide repeat motifs, including differentiation between prion strains \cdot
                                                                                                                                                                                                                                                                                                                                                                                                                Prion protein; subacute transmissible spongiform encephalopathy; ESST. Creutzfeld-Jakob disease; bovine spongiform encephalopathy; scrapie.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Octa-peptide motif repeated in human prion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB84521;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                Example 1;
                                                                                                                                      WPI; 2001-408079/43
                                                                                                                                                                     Deslys J,
                                                                                                                                                                                                                                           12-NOV-1999;
                                                                                                                                                                                                                                                                           13-NOV-2000;
                                                                                                                                                                                                                                                                                                             17-MAY-2001
                                                                                                                                                                                                                                                                                                                                               WO200135104-A1
                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB84521 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   preparation of antibodies including dimer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ω
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                                                                                                                                                                                                        COMMISSARIAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
8; Conser
                              Page 13; 51pp;
                                                                                                                                                                     Comoy E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                        Grassi J;
                                                                                                                                                                                                        ENERGIE ATOMIQUE.
                                  French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA
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0.027;
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The

present sequence represents an octa-peptide repeat motif of

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ARUSINT 4
ARUSINE AAUII825
ID AAUI
AC AAUI
AC AAUI
XX AUI
AC AAUI
XX Pric
CF Pric
KW Pric
KW Pric
KW Pric
KW Gere
KW Gere
KW Gere
KW Chran
XX Mamm
XX Key
FT Modi
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of subacute transmissible spongiform encephalopathy (ESST) caused by a strain of unconventional transmissible agent. The method comprises detecting abnormal prion protein in a biological sample. The sample is treated with at least one proteinase K while retaining at least some of the octapeptide repeats in the prion protein, then treatment with a ligand for octapeptide repeats and detecting any formation of a complex. The method is used to diagnose ESST, particularly (new variant) Creutzfeld-Jakob diseases, bovine spongiform encephalopathy and
polypeptide containing the sequence GlyTyrGlyGlnProHisGlyGly (A) or an analogue that is the retro-inverso isomer of (A). The sequence A is an octapeptide motif from the prion protein (PrP). The ligands are identified by binding assays with the peptide (A) or peptides containing (A). The ligands are used for detecting prion proteins (or prions) in
                                                                                                              Claim 1;
                                                                                                                                                           New ligands for prion proteins, useful prions and for treating prion-associat
                                                                                                                                                                                                                                      Hammond DJ,
                                                                                                                                                                                                                                                                                                  05-APR-2000;
                                                                                                                                                                                                                                                                                                                               05-APR-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chronic wasting disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             feline spongiform encephalopathy; bovine spongiform encephalopathy; transmissible mink encephalopathy; exotic ungulate encephalopathy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          prion-associated disease; Creutzfeldt-Jakob disease;
Gerstmann-Straussler-Scheinker disease; fatal familial insomnia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Prion protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Prion protein,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   scrapie.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        prion protein. The specification describes a method for the diagnosis
                                                                                                                                                                                                                                                                    (VITE-) VI TECHNOLOGIES INC
                                                                                                                                                                                                                                                                                                                                                               18-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 GWGQPHGG
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                                                                              invention relates to a ligand of less than 6 kD that binds
                                                                                                                                                                                                         2002-061944/08
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8; Consert
                                                                                                            Page 33; 47pp; English
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                                                                                                                                                       treating prion-associated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     octapeptide motif containing peptide
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                                                                                                                                                                                                                                      VR,
                                                                                                                                                                                                                                                                                                                                                                                                                       "Gly is amidated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Gly is acetylated"
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                                                                                                                                                                                                                                      Carbonell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          octapeptide motif;
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Pred. No. 0.034;
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                                                                                                                                                                                                                                      70,
                                                                                                                                                       for detection or removal or ed diseases, recognize a specific
                                                                                                                                                                                                                                      Shen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          scrapie;
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RESULT 5
AAU11856
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Best Local
polypeptide containing the sequence GlyTyrGlyGlnProHisGlyGly (A) or an analogue that is the retro-inverso isomer of (A). The sequence A is an octapeptide motif from the prion protein (PrP). The ligands are identified by binding assays with the peptide (A) or peptides containing (A). The ligands are used for detecting prion proteins (or prions) in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    scrapie, bovine or feline spongiform encephalopathy, transmissible mink or exotic ungulate encephalopathy, or chronic wasting disease. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              prion-associated diseases, especially Creutzfeldt-Jakob diseases (in iatrogenic, new variant, familial or sporadic forms), but also Gerstmann-Straussler-Scheinker disease, fatal familial insomnia,
                                                                   The invention
                                                                                           Disclosure; Page 10;
                                                                                                                     octapeptide
                                                                                                                                                                         WPI; 2002-061944/08.
                                                                                                                                                                                                                           (VITE-) VI
                                                                                                                                                                                                                                                   05-APR-2000;
                                                                                                                                                                                                                                                                             05-APR-2001;
                                                                                                                                                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chronic wasting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              prion-associated disease: Creutzfeldt-Jakob disease;
Gerstmann-Straussler-Scheinker disease; fatal familial insomnia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Prion protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Prion protein, PrP, octapeptide motif containing peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   biological or environmental samples, e.g. for diagnosis, also removing them from samples, for treating or retarding develop
                                                                                                                                    prions
                                                                                                                                                                                               Hammond DJ, Wiltshire VR, Carbonell
                                                                                                                                                                                                                                                                                                      18-OCT-2001.
                                                                                                                                                                                                                                                                                                                                WO200177687-A2
                                                                                                                                                                                                                                                                                                                                                                                              Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transmissible mink encephalopathy; exotic ungulate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  feline spongiform encephalopathy;
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8; Conser
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                                                                                                                    motif
                                                                                                                                             for prion proteins, useful
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                                                                  relates to a ligand of less than 6 kD that binds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           disease.
                                                                                                                                                                                                                                                                                                                                                                      /note=
16
                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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                                                                                          47pp; English.
                                                                                                                                                                                                                                                                                                                                                        "Gly is amidated"
                                                                                                                                                                                                                                                                                                                                                                                 "Gly is acetylated"
                                                                                                                                 prion-associated
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Pred. No.
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                                                                                                                                   diseases,
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                                                                                                                                                                                               Shen
                                                                                                                                               detection or removal or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23;
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                                                                                                                                 recognize
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       encephalopathy;
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RESULT 6
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Matches 8
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(PROT-) PROTEUS MOLECULAR DESIGN
                    03-DEC-1991;
10-JUL-1992;
                                                                           10-JUN-1993
                                                                                                                                 Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                        resistance
                                                                                                                                                                                                                                                                                                                                                                                                          human; sheep;
                                                                                                                                                                                                                                                                                                                                                                                                  immune system;
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nes 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                              prion; protein; region; frame shift; repeat: mutation; PrPc;
, subfragment; antibody; treatment; spongiform encephalopathy;
heep; cattle; cellular binding; aggregation; mammal; scrapie;
ystem; PrPsc; ratio-inverso peptide; enzymatic degradation;
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92GB-0014663.
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17
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Pred. No. 0.038;
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RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antigen; prion; protein; region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human; sheep;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immune system;
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ful for treatment and diagnosis of mammalian encephalopathies
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8; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  subfragment; antibody; treatment; spongiform encephalopathy; eep; cattle; cellular binding; aggregation; mammal; scrapie; stem; PrPsc; ratio-inverso peptide; enzymatic degradation;
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Pred. No. 0.042;
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RESULT 8
AAR38032
ID AAR3
XX AAR3
AC AAR3
AC Huma
XX Huma
XX Anti
KW FSa;
KW huma
KW resi
XX Synt
XX Synt
XX Synt
XX Synt
XX Synt
XX Synt
XX Misc
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Best Local (
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                                                                                                                                  Antigen; prion; protein; region; frame shift; repeat; mutation; rirc; FSa; FSb; subfragment; antibody; treatment; spongiform encephalopathy; human; sheep; cattle; cellular binding; aggregation; mammal; scrapie; immune system; PrPsc; ratio-inverso peptide; enzymatic degradation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    peptides sequences caused by a repeating section in region E having a nucleic acid coding sequence frame shift mutation of +1 (FSa) or -1 (FSb) (see also AAR38037-38). These peptides and antibodies raised against these may be used to treat or prevent spongiform encephalopathy in humans, sheep or cattle. They can be used to block cellular binding and aggregation of prion proteins and to stimulate the mammalian immune system. These peptides may be used to distinguish between the normal form of prion protein (PrPo) and the scrapic-associated form (PrPsc). These peptides may include rare or synthetic amino acids or a ration of protein (PrPsc) and the scrapic-associated form (PrPsc).
                  Misc-difference
                                                 Misc-difference
                                                                                                Synthetic
                                                                                                                                                                                                                            Human prion protein region E #2.
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10-JUL-1992;
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92GB-0014663
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 /note= "May be absent"
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AAR38035

AAR38035 standard;

protein;

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14-OCT-1993

(first entry)

AAR38035;

Prion protein region E #2

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                                                                                                                                                                                                                                                                                                                      New polypeptide(s) contg. antigenic site of prion protein - useful for treatment and diagnosis of mammalian encephalopathies e.g. Creutzfeld-Jacob disease and kuru
                                                                                                                                                                                                                                                                                                   Claim
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Misc-difference 15
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Misc-difference 14
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Misc-difference 5
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les 8; Conser
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                      1 GWGQPHGG 8
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                                                                                                                                                                                                                                                                                                Page 71; 82pp; English.
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                                               Conservative
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RESULT 10
AAY07999
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AC AAY07
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XX 08-JU
DT 08-JU
XX Prion
KW Prion
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                        DE19745443-A1
                                                                               Prion prote detection;
                                                                                                                         Bovine prion protein derived peptide
                                                                                                                                                      08-JUL-1999
                                                                                                                                                                                   AAY07999;
                                                                                                                                                                                                                AAY07999 standard;
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    e.g. Creutzfeld-Jacob disease and kuru
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10-JUL-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antigen; prion; protein; region; frame shift; repeat; mutation; PrPc; FSa; FSb; subfragment; antibody; treatment; spongiform encephalopathy; human; sheep; cattle; cellular binding; aggregation; mammal; scrapie; immune system; PrPsc; ratio-inverso peptide; enzymatic degradation;
                                                   Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                      degradation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1993-196994/24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (PROT-) PROTEUS MOLECULAR DESIGN LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 resistance.
                                                                                                                                                                                                                                                                                       7
                                                                                                                                                                                                                                                                                                                                              Local Similarity
es 8; Conserv
                                                                                                                                                                                                                                                                                                                 1 GWGQPHGG
                                                                                                                                                                                                                                                                                      protein; PrP
tion; bovine;
                                                                                                                                                                                                                                                                                                                                                                                                         26
                                                                                                                                                                                                                                                                                                                                             100.0%;
ilarity 100.0%;
Conservative (
                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                       14
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                                                                                            PrP;
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92GB-0014663.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92WO-GB02246
                                                                                                                                                                                                              protein; 42
                                                                                murine
                                                                                              human;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        English.
                                                                                            polyclonal antiserum;
                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                              Score 55; DE Pred. No. 0.0
                                                                                                                                                                                                                Ą
                                                                                                                            III.
                                                                                                                                                                                                                                                                                                                                                             0.06;
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                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                         Length 26;
                                                                                              immunoassay;
                                                                                                                                                                                                                                                                                                                                                Indels
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RESULT 11
AAW70280
В
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Best Local S
         01-MAY-1997;
06-FEB-1997;
24-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention describes a novel process for producing a polyclonal antiserum against a human or animal prion protein (PrP) which can be used in immunoassays for detecting PrP's. The method comprises (a) selecting a polypeptide that has a length of at least 10 amino acids and has an amino acid sequence at least 70% homologous to that of human, bovine or murine PrP in a region of at least 10 consecutive amino acids (b) binding a metal to the polypeptide by reaction with a metal compound and (c) injecting the metal-containing polypeptide into a host animal, optionally together with adjuvants, to induce production of a polyclonal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Diagnostic polyclonal antiserum specific for prion protein obtained by immunisation with metal-containing polypeptide % \left( 1\right) =\left\{ 1\right\} 
                                                                                                                                                 Region
                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                    06-NOV-1998
                                                                                                                                                                                                                                                                                                                                           AAW70280;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 4; 12pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-OCT-1997;
                                                        06-FEB-1998;
                                                                              13-AUG-1998
                                                                                                                                                                                   Region
                                                                                                                                                                                                Key
                                                                                                                                                                                                                                                                     Spinal cord;
                                                                                                                                                                                                                                                                                          Peptide sequences used to raise antibodies against prion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-OCT-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HERZ/) HERZOG-MESMER A
                                                                                                                                                                                                                                             immunological
                                                                                                                                                                                                                                                         3SE; scrapie;
                                                                                                                                                                                                                                                                                                                                                                                                                           4
                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GWGQPHGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
8; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; ilarity 100.0%; Conservative (
                                                                                                                                                                                                                                                        cattle; sheep; pig; bovine spongiform encephalopathy;
transmissable spongiform encephalopathy; TSE;
                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                            11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA;
                                                                                                                                                                                                                                              assay; scrapie
         971E-0000325.
971E-0000081.
971E-0000228.
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                                                        98WO-IE00007
                                                                                                                                                                                   Location/Qualifiers 28..61
                                                                                                                                                90..128
                                                                                                                                                            /note= "Synthetic sequence against prpSC"
                                                                                                                                       /note=
                                                                                                                                                                                                                                                                                                                                                                peptide;
                                                                                                                          "Synthetic sequence against prpSC"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                             prion protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 55;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.094;
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                                                                                                                                       raise antibody
                                                                                                                                                                          raise antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention claims to provide a method for detecting transmissable spongiform encephalopathies (TSE) in animals and in animal carcasses. The method comprises of an immunological assay whereby the animal test sample is reacted with a labelled antibody against scrapie prion protein (prpSC) and the amount of bound labelled antibody is then detected. The anti-prpSC antibodies used in the assay are raised against fragments of the present synthetic peptide shown. The peptide fragments preferred by the inventors are shown in the features table. The method is claimed to be useful when applied to samples, particularly a cross-section of the spinal cord, from cattle, sheep and pig carcasses for detection of bovine spongiform encephalopathy (BSE) or scrapie.
                                               (WALL-)
(BBSR-)
                       Hope
WPI; 2000-387880/33
                                                                                                               27-OCT-1999;
                                                                                                                                        25-MAY-2000.
                                                                                                                                                                WO200029850-A1
                                                                                                                                                                                                                 Disulfide-bond Modified-site
                                                                                                                                                                                                                                                                    Region
                                                                                                                                                                                                                                                                                 Key
                                                                                                                                                                                                                                                                                                       Mus sp
                                                                                                                                                                                                                                                                                                                               Mouse; prion protein;
bovine spongiform ence
                                                                                                                                                                                                                                                                                                                                                                      Mouse prion protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                               17-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                        AAB07316;
                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB07316 standard; protein; 208 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 3; Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Detecting pathogenic prion(s) in specific labelled antibody, used bovine spongiform encephalopathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1998-447377/38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  O'Connor
                                                                                    17-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ENFE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77
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8; Conser
                                                 BBSRC OFFICE.
                                                              WALLAC
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                       Barnard GJR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; ilarity 100.0%; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA;
                                                                                      98FI-0002481
                                                                                                              99WO-FI00897
                                                                                                                                                                                                                          /note= "Repeat region consisting of tundem repeats of repeat unit: PHGGGWGQ (AAB07319)"
                                                                                                                                                                                                                                                                    Location/Qualifiers 37..68
                                                                                                                                                                                         membrane
                                                                                                                                                                                    /note= "C-terminal phospho-inositol glycolipid
membrane anchor (-GPI)"
                                                                                                                                                                                                                                                                                                                               ein; transmissible spongiform encephalopathy;
encephalopathy; BSE diagnosis; TSE; PrP.
                       Birkett CR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 55; DE Pred. No. 0.3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               animal carcasses - by reaction with to detect those carrying agents for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and scrapie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 178;
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RESULT 13
AAB07318
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is the mouse prion protein (PrP) sequence. Conversion of the normal cellular form of PrP into an aggregated, incomplete isoform is implicated in the pathogenesis of Transmissible spongiform Encephalopathies (TSEs). Examples of TSEs include Bovine spongiform Encephalopathy (BSE), Scrapic, Creutzfeldt-Jakob disease (CJD) and Gerstmann-Straussler-Sheinker syndrome (GSS). The concentration of this protein in body fluid or tissue samples may be measured by an assay of the present invention, in which a presence of PrP indicates TSE. PrP antibody, which is then detected. The presence of PrP indicates TSE. PrP epitopes (AABO7320-B07326) are derived from the protease resistant core
                                                                                                                                (WALL-)
                                   Novel immunoassay for prion protein, used transmissible spongiform encephalopathies
                                                                                                      Hope J,
                                                                                                                                                                                                                                                                                                                     Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                            Human; prion protein;
bovine spongiform enc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human prion protein sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB07318 standard; protein; 208 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                             WPI; 2000-387880/33.
                                                                                                                                                                       17-NOV-1998;
                                                                                                                                                                                                27-OCT-1999;
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                                                                                                                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                                                                                                            Region
                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of PrP that is occluded when the PrP is in an aggregated state.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel immunoassay for prion protein, used for the determination transmissible spongiform encephalopathies in bovines \,\cdot\,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41 GWGQPHGG 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GWGQPHGG
                                                                                                                                             WALLAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
8; Conserv
                                                                                                                                BBSRC OFFICE.
                                                                                                    Barnard GJR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         208 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Page 41-42; 50pp; English.
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                                                                                                                                                                       98FI-0002481
                                                                                                                                                                                                 99WO-FI00897
                                                                                                                                                                                                                                                                                                                /note= "Repeat region consisting of tandem repeats
of repeat unit: PHGGGWGQ (AAB07319)"
157...192
                                                                                                                                                                                                                                                                             /note= "C-terminal phospho-inositol glycolipid
membrane anchor (-GPI)"
                                                                                                                                                                                                                                                                                                         208
                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers 29..69
                                                                                                                                                                                                                                                                                                                                                                                                                            ein; transmissible spongiform encephalopathy;
encephalopathy; BSE diagnosis; TSE; PrP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
                                                                                                      Birkett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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Pred. No. 0.43;
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                                     for the determination
in bovines -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                208;
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Disclosure;

Page 43-44; 50pp; English

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RESULT 14
AAB07327
   Query Match
Best Local :
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The present sequence is the mouse prion protein (PrP) sequence. Conversion of the normal cellular form of FrP into an aggregated, insoluble isoform is implicated in the pathogenesis of Transmissible Spongiform Encephalopathies (TSEs). Examples of TSEs include Bovine Spongiform Encephalopathy (BSE), scrapie, Creutzfeldt-Jakob disease
                                                                                                                                             New immunoassay for prion protein, used for determination transmissible spongiform encephalopathies in mammals, compspecific capture antibody -
                                                                                                                                                                                                                                                                                           (WALL-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Key
Region
                                                                                                              Disclosure;
                                                                                                                                                                                                                      WPI; 2000-399778/34
                                                                                                                                                                                                                                                        Hope J,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mouse;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        prion protein; transmissible spongiform encephalopathy;
spongiform encephalopathy; TSE diagnosis; PrP.
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8; Conser
                                                                                                                                                                                                                                                                                                              WALLAC
                                                                                                                                                                                                                                                                                           BBSRC
                                                                                                                                                                                                                                                        Barnard GJR,
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                                                                                                            Page 41-42; 50pp; English.
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                                                                                                                                                                                                                                                                                           OFFICE.
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of repeat unit: PHGGGWGQ (AAB07319)"
156..191
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membrane anchor (-GPI)"
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          The present sequence is the human prion protein (PrP) sequence. Conversion of the normal cellular form of PrP into an aggregated, insoluble isoform is implicated in the pathogenesis of Transmissible spongiform Encephalopathies (TSEs). Examples of TSEs include Bovine Spongiform Encephalopathy (BSE), scrapie, Creutzfeldt-Jakob disease (CJD) and Gerstmann-Straussler-Sheinker syndrome (GSS). The concentration of this protein in body fluid or tissue samples may be measured by an assay of the present invention, in which a PrP epitope is captured by an antibody, which is then detected. The presence of PrP indicates TSE. PrP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CJD) and Gerstmann-Straussler-Sheinker syndrome (GSS). The concentration of this protein in body fluid or tissue samples may be measured by an assay of the present invention, in which a PrP epitope is captured by an antibody, which is then detected. The presence of PrP indicates TSE. PrF epitopes (AAB07320-B07326) are derived from the protease resistant core of PrP that is occluded when the PrP is in an aggregated state.
                                                                                                                                                                                 New immunoassay for prion protein, used for
transmissible spongiform encephalopathies
specific capture antibody -
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(BBSR-)
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                                                                                                                                                      Disclosure; Page 43-44; 50pp; English.
                                                                                                                                                                                                                                            WPI;
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                                                                                                                                                                                                                                                                                                                                            17-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; prion protein; transmissible spongiform encephalopathy;
bovine spongiform encephalopathy; TSE diagnosis; PrP.
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8; Conser
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(AAB07320-B07326) are derived
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208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Repeat region consisting of tandem repeats
of_repeat unit: PHGGGWGQ (AAB07319)"
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membrane anchor (-GPI)"
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CC of PEP that is occluded when the PPP is in an aggregated state.

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Sequence 208 AA;

Sourcy Match 100.0%; Score 55; DB 21; Length 208;

MATCHES 6; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

OY 1 GNOPHOG 8

Db 34 GNOPHOG 41

Job time: 36.4545 accs 3, 2003, 15:28:34
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Result
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Maximum DB seq length: 2000000000
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              I number of hits satisfying chosen parameters:
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Copyright (c) 1993 - 2003 Compugen Ltd
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prion-related protimajor prion proteimajor prion prion
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RESULT 2 \$71041 major prion protein - black-handed spider monkey (fragment) C:Species: Ateles geoffroyi (black-handed spider monkey) C:Date: 27-Oct-1996 #sequence_revision 07-Feb-1997 #text_change 13-Aug-1999 C:Accession: \$71041; \$53630 R:Schatzl, H.M. submitted to the EMBL Data Library, April 1994 A:Reference number: \$71041 A;Accession: \$73634 A;Residues: 1-232 <sch> A;Residues: 1-232 <sch> A;Cross-references: EMBL:008309; NID:9474376; PIDN:AAC50097.1; PID:9474377 R;Schaetzl, H.M.; da COsta, M.; Taylor, L.; Cohen, F.E.; Prusiner, S.B. J. Mol. Biol. 245, 362-374, 1995 A;Title: Prion protein gene variation among primates, A;Reference number: \$53614; MUID:95139066; PMID:7837269 A;Accession: \$53630 A;Status: nucleic acid sequence not shown A;Residues: 1-194, 'R. 196-231 <scw> A;Cross-references: EMBL:008309 C;Keywords: amyloid; brain; glycoprotein; lipoprotein; prion; scrapie; transi</scw></sch></sch>	RESULT 1 A53892 prion-related protein - rat (fragment) C:Species: Rattus norvegicus (Norway rat) C:Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 13-Aug-1999 C:Accession: A53892 R:Liao, Y.C.; Tokes, Z.; Lim, E.; Lackey, A.; Woo, C.H.; Button, J.D.; Claws(Lab. Invest. 57, 370-374, 1987 A;Title: Cloning of rat "prion-related protein" cDNA. A;Reference number: A53892 A;Status: preliminary A;Molecule type: mRNA A;Ccession: A53892 A;Cross-references: GB:M2031; NID:g206391; PIDN:AAA41947.1; PID:g206392 C;Superfamily: major prion protein Query Match Best Local Similarity 100.0%; Score 55; DB 2; Length 226; Best Local Similarity 100.0%; Pred. No. 0.069; Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps Qy 1 GWGQPHGG 8 - - - -	30 55 100.0 254 2 A23544 major prion protei 31 55 100.0 256 2 JU0268 major prion protei 32 55 100.0 256 2 S37149 prion protein - 90 33 55 100.0 256 2 A54281 major prion protein 34 55 100.0 257 2 A23545 major prion protei 35 55 100.0 257 2 JQ1900 major prion protei 36 55 100.0 260 2 S53629 major prion protei 37 55 100.0 264 2 S37137 prion protein - 91 38 55 100.0 264 2 A54330 prion protein protei 40 41 74.5 395 2 T08350 prion protein protei 41 41 74.5 521 2 E64862 42 40 72.7 327 2 E87218 probable membrane 43 40 72.7 1161 2 T45294 protein B0213.5 [i 44 39 70.9 69 2 B89016 protein B0213.5 [i 51 00.0 264 2 A54300 protein B0213.5 [i 52 00.0 264 2 A54300 protein B0213.5 [i 53 00.0 264 2 A54300 protein B0213.5 [i 54 00.0 264 2 A54300 protein B0213.5 [i 55 00.0 264 2 A54300 protein B0213.5 [i 56 00.0 264 2 A54300 protein B0213.5 [i 57 00.0 264 2 A54300 protein B0213.5 [i 58 00.0 26
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Query Match

100.0%;

Score 55;

DB 2

Length 232;

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A;Molecule type: DNA
A;Residues: 1-203,'R',205-240 <SCW>
A;Cross-references: EMBL:U08303
C;Superfamily: major prion protein
C;Keywords: amyloid; brain; glycoprotein; lipoprotein; prion; scrapie;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: DNA
A;Residues: 1-202, 'E',204-239 <SCW>
A;Residues: 1-202, 'E',204-239 <SCW>
C;Coss references: EMBL:U08293; NID:g474344; PIDN:AAC50082.1; PID:g474
C;Superfamily: major prion protein
C;Keywords: amyloid; brain; glycoprotein; lipoprotein; prion; scrapie;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C:Species: Aotus trivirgatus (douroucoul, night monkey, owl monkey)
C:Date: 28-Oct-1996 #sequence_revision 07-Feb-1997 #text_change 13-Aug-1999
C:Accession: S53633; S71042
R:Schaetzl, H.M.; da Costa, M.; Taylor, L.; Cohen, F.E.; Prusiner, S.B.
J. Mol. Biol. 245, 362-374, 1995
A:Title: Prion protein gene variation among primates.
A:Reference number: S53614; MUID:95139066; PMID:7837269
A:Accession: S53633
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A;Title: Prion protein gene variation among primates A;Reference number: S53614; MUID:95139066; PMID:7837 A;Accession: S53621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       major prion protein - mandrill (fragment)
(;Species: Papio sphinx, Mandrillus sphinx (mandrill)
C;Date: 27-Oct-1996 #sequence_revision 14-Feb-1997 #t
C.Coccession: S71056; S53621
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R:Schaetzl, H.M.; da Costa, M.; Taylor, L.; Cohen, F.E.; Prusiner, S.B.
                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-241 <SCH>
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submitted to the EMBL Data
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                                                                         100.0%; Score 55; DB 2; 100.0%; Pred. No. 0.073;
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Pred. No.
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                                                           Mismatches
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R;Schatzl, H.M.
submitted to the EMBL Data
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A;Cross-references: EMBL:U08312
C;Superfamily: major prion protein
C;Keywords: amyloid; brain; glycoprotein; lipoprotein; prion; scrapie; transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           major prion protein - Callicebus moloch (fragment)
C;Specles: Callicebus moloch
C;Date: 27-Oct-1996 #sequence_revision 07-Feb-1997 #text_change 13-Aug-1999
C;Accession: S71048; S53632
                                                                                                                                                        C;Superfamily: major prion protein
C;Keywords: amyloid; brain; glycoprotein;
                                                                                                                                                                                       A;Molecule type: DNA
A;Residues: 1-10,'V',12-202,'E',204-245 <SCW>
A;Cross-references: EMBL:U08291; NID:g474340; PIDN:AAC50080.1; PID:g474341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          major prion protein - green monkey
C;Species: Cercopithecus aethiops (green monkey, grivet)
C;Date: 28-Oct-1996 #sequence_revision 07-Feb-1997 #text
C;Accession: S53627; S71043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Title: Prion protein gene variation among primates. A; Reference number: S53614; MUID:95139066; PMID:7837269 A; Accession: S53632
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A; Residues: 1-245 <SCH>
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J. Mol. Biol. 245, 362-374, 1995
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J. Mol. Biol. 245, 362-374, 199
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A; Residues: 1-241 <SCH>
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                                                                                                    Query Match
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                                                                               Conservative
63
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                                                                                             100.0%; Score 55;
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Pred. No. 0.073;
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major prion protein - common marmoset (;Species: Callithrix jacchus (common marmoset) C;Species: Callithrix jacchus (common marmoset) C;Date: 28-Oct-1996 #sequence_revision 07-Feb-1997 #text_change 13-Aug-1999 C;Accession: S53634; S71047 R;Schaetzl, H.M.; da Costa, M.; Taylor, L.; Cohen, F.E.; Prusiner, S.B. J. Mol. Biol. 245, 362-374, 1995
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A;Title: Infectious amyloid precursor gene sequences in primates used for experimental precursor gene sequences in primates used for experimental precursor number: 136907; MUID:95083661; PMID:7991600
A;Accession: I61848
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C;Species: Saimiri sciureus (common squirrel monkey)
C;Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 13-Aug-1999
C;Accession: I61848
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C;Species: Cercopithecus dianae
C;Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 13-Aug-1999
                   A; Molecule type: DNA
A; Residues: 1-252 <S(
                                                       A; Status: nucleic acid sequence not shown
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A:Residues: 8-10,'L',12-202,'R',204-239
:ss-references: EMBL:U08292
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R;Schaetzl, H.M.; da Costa, M.; J
J. Mol. Biol. 245, 362-374, 1995
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A; Residues: 1-245 <SCH>
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R; Schatzl, H.M.
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Cross-references: EMBL:015165; NID:9595852; PIDN:AAA68636.1; PID:9595853
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EMBL: U08304
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Pred. No. 0.074;
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                                                                                                  PMID: 7837269
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C;Accession: S53631; S71044
R;Schaetzl, H.M.; da Costa, M
J. Mol. Biol. 245, 362-374, 19
A;Title: Prion protein gene va
A;Reference number: S53614; MI
A;Accession: S53631
A; Gene: PrP
C; Superfamily: major prion protein
C; Keywords: disulfide bond; prion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Schatzl, H.M.
submitted to the EMBL Data Library,
                                                                        A;MoLecule type: DNA
A;Residues: 1-252 <LOP>
A;Cross-references: GB:U28334; NID:q1490412; PIDN:AAC48697.1;
C;Comment: This protein is a cellular protein, it is involved
                                                                                                                                                                                                                                                 C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 11-Apr-1997 #sequence_revision 09-May-1997
C;Accession: JC6175
                                                                                                                                                                                                                                                                                                                                                                                                                                      QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Superfamily: major prion protein
C;Keywords: amyloid; brain; glycop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               submitted to the EMBL Data Library, A; Reference number: S71041 A; Accession: S71044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Cebus apella (brown capuchin, black-capped capuchin)
C;Date: 28-Oct_1996 #sequence_revision 07-Feb-1997 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:U08304; NID:g474366; PIDN:AAC50092.1; PID:g474367 C;Superfamily: major prion protein C;Keywords: amyloid; brain; glycoprotein; lipoprotein; prion; scrapie; transmembrane
                                                            C; Genetics:
                                                                                                                                                   A;Title: Characterization of A;Reference number: JC6175; RA;Accession: JC6175
                                                                                                                                                                                                        R; Loftus, B.; Rogers, M.
Gene 184, 215-219, 1997
                                                                                                                                                                                                                                                                                                       prion protein - rabbit
                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule typé: DNA
A; Residues: 1-209, 'E', 211-252 <SCW>
A; Cross_references: EMBL:U08295; NI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Residues: 1-252 <SCH>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: nucleic acid sequence not shown
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A; Residues: 1-209, 'E', 211-252 <SCW>
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Matches
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Matches 8; Conser
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8; Conser
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ilarity 100.0%;
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1995
                                                                                                                                                                         f a prion protein (PrP) gene MUID:97183665; PMID:9031631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     glycoprotein; lipoprotein; prion;
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Pred. No. 0.076;
Mismatches
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Pred. No. 0.076;
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in the neuro
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R;Brown, P.; Goldfarb, L.G.; McComble, W.R.;
Neurology 42, 422-427, 1992
A;Title: Atypical Creutzfeldt-Jakob disease
A;Reference number: 158135; MUID:92140671; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: DNA
A;Residues: 8-240 <RE3>
A;Residues: 8-240 <RE3>
A;Cross-references: GB:M81930; NID:g190519; PIDN:AAB59443.1; PID:g190520
A;Cross-references: L.G.; McCombie, W.R.; Nieto, A.; Squillacote, D.;
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C:Date: 25-Oct-1987 #sequence_revision 12-Apr-1996 #text_change 16-Jun-2000
C:Date: 25-Oct-1987 #sequence_revision 12-Apr-1996 #text_change 16-Jun-2000
C:Accession: A24173; A05017; S14078; I59322; I68597; I58135; I59184;
R:Kretzschmar, H.A.: Stowring, L.E.; Westaway, D.; Stubblebine, W.H.; Prusine DNA 5, 315-324, 1986
A:Title: Molecular cloning of a human prion protein cDNA.
A:Title: Molecular cloning of a human prion protein cDNA.
A:Gerence number: A24173; MUID:86300093; PMID:3755672
Cession: A24173
A;Reference number: I58135;
A;Accession: I58135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Title: Deletion in the prion protein gene A,Reference number: I54322; MUID:93250789; FA,Accession: I54322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; MoLecule type: protein
A.Residues: 58-72, 'x', 74-76, 'xx', 74-76, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: Amyloid protein of Gerstmann-Straeussler-Scheinker disease (Indiana kindred) A;Reference number: S14078; MUID:91160504; PMID:1672107 A;Accession: S14078
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A;NOTE: The deletion may be a polymorphism; the alternative deletion of 82-89
R;Liao, Y.C.J.; Lebo, R.V.; Clawson, G.A.; Smuckler, E.A.
Science 233, 364-367, 1986
A;Reference number: A05017; MUID:86261778; PMID:3014653
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N;Alternate names: 11K amyloid protein; 27-30K sialoglycoprotein; PrP 27-30;
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A; Residues: 1-80,89-253 < PUC>
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Am. J. Hum. Genet. 49, 320-329,
                                                                                                                                                                                                                           A; Molecule type: DNA
                                                                                                                                                                                                                                                                        A;Status: preliminary; translated from GB/EMBL/DDBJ
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A: Residues: 9-83,92-240 < RES>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1;Status: preliminary; translated from GB/EMBL/DDBJ
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Knopman, D.S.; List, J.F.; Olson, K.; Frey, W.H.
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                                                             G.D.; Wills,
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                                                             P.R.
                                                                                                                                                                                                                                                                                                                                                                  major prion protein precursor - chimpanzee
C;Species: Pan troglodytes (chimpanzee)
C;Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 13-Aug-1999
C;Accession: I61847; S71060; S53615
                                                                                                          A; Reference number: I36907; A; Accession: I61847
                                                                                                                                                                                                                           A; Title:
                                                                                                                                                                                                                                                                  R;Cervenakova, L.; Brown, P.; Goldfarb, L.G.; Nagle, J.; Proc. Natl. Acad. Sci. U.S.A. 91, 12159-12162, 1994
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           A; Molecule
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                                                                                                                                                                                                                     Infectious amyloid
                                                             translated
           type: DNA
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from

GB/EMBL/DDBJ

precursor gene sequences in MUID:95083661; PMID:7991600

primates used

for experimenta

Pettrone,

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A;Introns: #status absent
A;Note: one intron occurs before the initiator codon
A;Note: one intron occurs before the initiator codon
A;Note: this gene is associated with Creutzfeld-Jakob disease (CJD), Gerstmann-Straus
C;Superfamily: major prion protein
C;Keywords: amyloid; blocked carboxyl end; brain; glycoprotein; lipoprotein; phosphat
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-230/Product: major prion protein #status predicted <MAT>
F;54-92/Region: 8-residue repeats (P-H-G-G-W-G-O)
                                                                                                                                                                                                                         F;231-253/Domain: carboxyl-terminal propeptide #status predicted <C F;179-214/Disulfide bonds: #status predicted F;181.197/Binding site: carbohydrate (Asn) (covalent) #status predi F;230/Modified site: GPI-anchor ethanolamine amidated carboxyl end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GDB:120720; OMIM:176640; OMIM:137440 A;Map position: 20pter-20p12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: Transmissible familial Creutzfeldt-Jakob disease associated with five, seven A;Reference number: I59184; MUID:92073400; PMID:1683708
                                                                                                                                                                                                                                                                                                                                            F;112-134/Domain: transmembrane #status predicted <TM1>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:S71208; NID:g239877; PIDN:AAB20521.1;
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56 GWGQPHGG
                                                      1 GWGQPHGG
                                                                                                               Similarity
8; Conserv
                                                                                                            100.0%; ilarity 100.0%; Conservative (
63
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                                                                                                                                                                   Score 55;
                                                                                                                                          Pred. No.
                                                                                                            Mismatches
                                                                                                                                          0.076;
                                                                                                                                                                         DB 1;
                                                                                                                                                                      Length 253;
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                                                                                                            Gaps
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A;Title: Infectious amyloid precursor gene sequences in A;Reference number: I36907; MUID:95083661; PMID:7991600 A;Accession: I37032 A;Cross-references: EMBL:U15166; NID:g563208; PIDN:AAA68633.1; C;Superfamily: major prion protein_ A; Molecule type: DNA A; Residues: 1-253 <RES> R;Cervenakova, L.; Brown, P.; Goldfarb, L.G.; Nagle, J.; Proc. Natl. Acad. Sci. U.S.A. 91, 12159-12162, 1994 major prion protein precursor - gorilla C;Species: Gorilla gorilla (gorilla) C;Date: 31-May-1906 #sequence_revision C;Accession: 137032 56 GWGQPHGG 1 GWGQPHGG preliminary; translated Similarity 8; Conser 100.0%; ilarity 100.0%; Conservative (prion protein 0; from Score 55; DB 2; Pred. No. 0.076; Mismatches GB/EMBL/DDBJ 31-May-1996 #text_change 13-Aug-1999 'n Length 253; primates used Pettrone, PID: 9563209 0 K.; Rubenstein, Gaps for experimenta 0 **R**

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A;Molecule type: DNA
A;Residues: 1-210,'R',212-253 <SCH>
A;Cross-references: EMBL:U08296
C;Superfamily: major prion protein
C;Superfamily: major prion; glycoprotein; lipoprotein; prion; scrapie; transmembrane pro
Search completed: January 3, 2003, 15:33:13 Job time: 13.2727 secs
                                                                                                         В
                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:U08308; NID:g474374; PIDN:AAC50096.1; PID:g474375 A;NOte: the source was designated as Symphalangus syndactylus A;Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1994 A;Note: the mid-potition protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Title: Prion protein gene variation among primates. A; Reference number: S53614; MUID:95139066; PMID:7837269 A; Accession: S53635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   prion protein - siamang
C;Species: Hylobates syndactylus (siamang)
C;Date: 15-Jul-1995 #sequence_revision 19-Apr-1996 #text_change 13-Aug-1999
C;Accession: S53635
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A;Residues: 1-23 <SGW>
A;Residues: 1-23 <SGW>
A;Coss-references: EMBL.U08296; NID:9474350; PIDN:AAC50085.1; PID:9474351
A;Cross-references: EMBL.U08296; NID:9474350; DID:95.25085.1; PID:9474351
Cohen, F.E.; Prusiner, S.B.
J. Mol. Biol. 245, 362-374, 1995
A;Title: Prion protein gene variation among primates.
A;Reference number: S53614; MUID:95139066; PMID:7837269
A;Accession: S53615
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R;Schatzl, H.M.

A;Reference number: S71041
A;Accession: S71060
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56 GWGQPHGG 63
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                                                                                                                                                                                                           0;
                                                                                                                                                                                                         Score 55; DB 2; Length 253; Pred. No. 0.076; ; Mismatches 0; Indels
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Maximum Match 100%
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Maximum DB
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                                                                                                                   P40250 cercopithec
Q95172 cercopithec
Q95174 cercopithec
Q95176 cercocebus
P51446 ateles pani
P40247 callithrix
P40249 cebus apell
Q95211 cryctolagus
P40252 gorilla gor
P40252 gorilla gor
P04156 homo sapien
P40254
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P40255 mandrillus
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1 colobus gue
2 gorilla gor
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EMBL; U75382;
HSSP; P04925;
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                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                der Kuyl A.C., Dekker J.T., Submitted (NOV-1996) to the
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01-NOV-1997 (Re
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NCBI_TaxID=36222, 9546;
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Fukarvota; Metazoa; Chordata;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: BELONGS TO THE PRION FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBUNIT: PRP
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E FUNCTION OF PRP IS NOT KNOWN. PRP IS ENCODED IN THE
AND IS EXPRESSED BOTH IN NORMAL AND INFECTED CELLS.
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SMART; SM00157; PRP; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases:
-i- FUNCTION: THE FUNCTION OF PRP IS NOT KNOWN. PRP IS ENCODED IN THE
-HOST GENOME AND IS EXPRESSED BOTH IN NORMAL AND INFECTED CELLS.
-i- SUBUNIT: PRP HAS A TENDENCY TO AGGREGATE YIELDING POLYMERS CALLED
                                                                                                                                                                                                                                                                                                                                                                                                                                                               der Kuyl A.C., Dekker J.T., Submitted (NOV-1996) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cercopithecinae;
NCBI_TaxID=9565;
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Eukaryota; Metazoa; Chordata; Craniata; Ve
Mammalia; Eutheria; Primates; Catarrhini;
Cercopithecinae; Theropithecus.
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                                                                                                                                                                                                                                                                                                                      SIMILARITY: BELONGS TO THE PRION FAMILY.
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MAJOR PRION PROTEIN.
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
4 X 8 AA TANDEM REPEATS OF P-H-G-G-G-G.
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                                                                                                                        GPI-anchor;
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                                                                                                BY SIMILARITY
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                    (CJD), GERSTMANN-STRAUSSLER SYNDROME
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                                                                                                                                                                                                                                             (See http://www.isb-sib.ch/announce/
                                                                                                                        Repeat;
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                                     (POTENTIAL).
OF P-H-G-G-G-W-G-
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Best Local
                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                           Schatzl H.M., Dacosta M., Taylor L., Cohen F.E., Prusiner S.E "Prion protein gene variation among primates.";
J. Mol. Biol. 245:362-374(1995).
-i- FUNCTION: THE FUNCTION OF PRP IS NOT KNOWN. PRP IS ENCODE HOST GENOME AND IS EXPRESSED BOTH IN NORWAL AND INFECTED-
-i- SUBUNIT: PRP HAS A TENDENCY TO AGGREGATE YIELDING POLYMEN
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SEQUENCE
                        REPEAT
REPEAT
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                                                                                                                                                                         InterPro; IPR000817; Prion.
Pfam; PF00377; prion; 1.
SMART; SM00157; PRP; 1.
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REPEAT
                                                                                CARBOHYD
                                                                                                                                                                                                                      EMBL; U08293; AAC50082.1; -.
                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                       entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                            DOMAIN
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                                                                                                                            Prion; Brain;
NON_TER
                                                                                                                                                   PROSITE; PS00291; PRION_1; 1. PROSITE; PS00706; PRION_2; 1.
                                                                                                                                                                                                            HSSP; P04925;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=95139066; PubMed=7837269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor DISEASE: PRP IS FOUND IN HIGH QUANTITY IN THE BRAIN OF HUMANS ANIMALS INFECTED WITH THE DEGEMERATIVE NEUROLOGICAL DISEASES FOR CREUTZFELDT-JAKOB DISEASE (CJD), GERSTMANN-STRAUSSLER SYNDROME
                                                                                                                                                                                                                                                                                                                                     SIMILARITY: BELONGS TO THE PRION FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                          SUBUNIT: PRP
                                                                                                                                                                                                                                                                                                                                              (GSS), SCRAPIE, BOVINE SPONGIFORM ENCEPHALOPATHY (BSE), TRANSMISSIBLE MINK ENCEPHALOPATHY (TME), ETC.
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8; Conserv
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BY SIMILARITY
MAJOR PRION PROTEIN.
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
5 X 8 AA TANDEM REPEATS OF P-H-G-G-G-G.
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                     (CJD), GERSTMANN-STRAUSSLER SYNDROME
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Aotinae; Aotu
                                                          (POTENTIAL).
OF P-H-G-G-G-W-G
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Best Local
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-!- FUNCTION: THE FUNCTION OF PRP IS NOT KNOWN.
                                                                                                                                                                                                                                                          PROSITE; PS00
Prion; Brain;
                                                                                                                                                                                                                                                                                                                         Pfam; PF00377; prion; : SMART; SM00157; PRP; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long modified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HOST GENOME AND IS EXPRESSED BOTH IN NORMAL AND IT IS UBUNIT: PRP HAS A TENDENCY TO AGGREGATE YIELDING "RODS".
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Callicebus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRNP
                                                                                                                                   CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000817; Prion.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=95139066; PubMed=7837269;
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nes 8; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor. DISEASE: PRP IS FOUND IN HIGH QUANTITY IN THE BRAIN OF HUMANS / ANIMALS INFECTED WITH THE DEGENERATIVE NEUROLOGICAL DISEASES KUCRUTZFELDT-JAKOB DISEASE (CJD), GERSTMANN-STRAUSSLER SYNDROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSMISSIBLE MINK ENCEPHALOPATHY (TME), ETC. SIMILARITY: BELONGS TO THE PRION FAMILY.
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    Created)
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BY SIMILARITY.
MAJOR PRION PROTEIN.
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
5 X 8 AA TANDEM REPEATS OF P-H-G-G-W-G-Q.
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                                                                                                                                                                                                                                                          Repeat;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL outstation
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L outstation -
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Matches 8; Conserv
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01-FEB-1995
01-FEB-1995
01-OCT-1996
                                                               DISULFID CARBOHYD
                                                                                                   SIGNAL
CHAIN
PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Prion protein gene variation among primates.";

J. Mol. Biol. 245:362-374(1995).

-I- FUNCTION: THE FUNCTION OF PRP IS NOT KNOWN. PRP IS ENCODED IN THE HOST GENOME AND IS EXPRESSED BOTH IN NORMAL AND INFECTED CELLS.

-I- SUBUNIT: PRP HAS A TENDENCY TO AGGREGATE YIELDING POLYMERS CALLED
                                                                                                                                         SMART; SM00157; rns, SMART; SM00157; rns, No. 1; 1.

PROSITE; PS00706; PRION_2; 1.

PROSITE; PS00706; PRION_1; GPI-anchor; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

MEDLINE-95139066; PubMed-7837269;
Schatzl H.M., Dacosta M., Taylor L., Cohen F.F.
Schatzl H.M., Dacosta M., Taylor L., Cohen F.F.
                                                                                                                                                                                                                                                                entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                           use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mandrillus sphinx (Mandrill) (Papio sphinx).
Eukaryota; Metazoa; Chordata; Craniata; Vert
Mammalia; Eutheria; Primates; Catarrhini; Ce
Cercopithecinae; Mandrillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Major prion PRNP.
                                                                                       LIPID
                                                                                                                                                                                          Pfam; PF00377; prion; 1. SMART; SM00157; PRP; 1.
                                                                                                                                                                                                                              EMBL; U08303; AAC50091.1; -. HSSP; P04925; 1AG2.
                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                REPEAT
                                        DOMAIN
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                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                                                 SUBCELULIAR LOCATION: Attached to the membrane by a GPI-anchor. DISEASE: PRP IS FOUND IN HIGH QUANTITY IN THE BRAIN OF HUMANS ANIMALS INTECTED WITH THE DECEMERATIVE REUROLOGICAL DISEASES K(CREUTZFELDT-JAKOB DISEASE (CJD), GERSTMANN-STRAUSSLER SYNDROME (GSS), SCRAPIE, BOVINE SPONGIFORM ENCEPHALOPATHY (BSS), TRANSMISSIBLE MINK ENCEPHALOPATHY (TME), ETC.
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                                                                                                                                                                                                                                                                                                                              the Swiss Institute of Bioinformatics
                                                                                                                                                                                                                    IPR000817; Prion.
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(Rel. 31, Last sequence update)
(Rel. 34, Last annotation updat
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                                                                                                                MAJOR PRION PROTEIN
                                                                                                                            BY SIMILARITY
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orimates.":
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RESULT 7
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Best Local :
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16-OCT-2001
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NON_TER
SEQUENCE
            DISULFID CARBOHYD
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                                                                                                                           InterPro; IPR000817; Prion. Pfam; PF00377; Prion; 1. PRINTS; PR00341; PRION. SMART; SM00157; PRP; 1.
                                                                                                                                                                                            EMBL; U08291; AAC50080.1; -.
                                                                                                                                                                                                                                                        the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Prion protein gene variation J. Mol. Biol. 245:362-374(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cercopithecus diana (Diana monkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                      TIPID
                                                                                                                                                                               EMBL; U08292; AAC50081.1; HSSP; P04925; 1AG2.
                                                                                                                                                                                                                                            modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                      + +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cercopithecus aethiops (Green monkey) (Grivet), and Cercopithecus diana (Diana monkey).
                                                    PROPEP
                                                              CHAIN
                                                                            SIGNAL
                                                                                        Prion;
                                                                                                    PROSITE; PS00291; PRION_1; PROSITE; PS00706; PRION_2;
                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                  between
                                                                                                                                                                                                                                                                                                               This
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE~95139066; PubMed~7837269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cercopithecinae; Cercopithecus.
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FUNCTION: THE FUNCTION OF PRP IS NOT KNOWN. PRP IS HOST GENOME AND IS EXPRESSED BOTH IN NORMAL AND IN SUBUNIT: PRP HAS A TENDENCY TO AGGREGATE YIELDING "RODS".
                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor. DISEASE: PRP IS FOUND IN HIGH QUANTITY IN THE BRAIN OF HUMANS A ANIMALS INFECTED WITH THE DEGENERATIVE NEUROLOGICAL DISEASES KU CREUTZFELDT-JAKOB DISEASE (CJD), GERSTMANN-STRAUSSLER SYNDROME
                                                                                                                                                                                                                                                                                                                                       SIMILARITY: BELONGS TO THE PRION FAMILY.
                                                                                                                                                                                                                                                                                                                                                 (GSS), SCRAPIE, BOVINE SPONGIFORM ENCEPHALOPATHY (BSE), TRANSMISSIBLE MINK ENCEPHALOPATHY (TME), ETC.
                                                                                                                                                                                                                                                                                               SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
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241
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(Rel. 31, Last sequence update)
(Rel. 40, Last annotation update)
(Rel. 40, Precursor (PrP) (PrP27-30)
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N-LINKED (GLCN
                                                                                        GPI-anchor;
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                                                              MAJOR PRION PROTEIN
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among primates.";
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Pred.
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Best Local S
Matches 8
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           DISULFID CARBOHYD
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REPEAT
  CARBOHYD
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                                                                                          Prion;
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SMART; SM00157; PRP; 1
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                                                                                                                                                                                                                              the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                 between
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                                                                                                                                                                                                                                                                                                                                                                                                                            der Kuyl A.C., Dekker J.T., Submitted (NOV-1996) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cercopithecinae; Cercopithecus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cercopithecus
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15-JUL-1998
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01-NOV-1997 (Re
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                                                                                                     PROSITE;
                                                                                                                                                  InterPro;
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                                                                                                                                                                                                         tities requires a license agreement (S send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor. DISEASE: PRP IS FOUND IN HIGH QUANTITY IN THE BRAIN OF HUMANS A ANIMALS INFECTED WITH THE DEGENERATIVE NEUROLOGICAL DISEASES KUCRUTZFELDT-JAKOB DISEASE (CJD), GERSTMANN-STRAUSSLER SYNDROME
                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: THE FUNCTION OF PRP IS NOT KNOWN. PRP IS ENCODE HOST GENOME AND IS EXPRESSED BOTH IN NORMAL AND INFECTED SUBURIT: PRP HAS A TENDENCY TO AGGREGATE YIELDING POLYMER
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                                                                                                                                                                                                                                                                                                            (GSS), SCRAPIE, BOVINE SPONGIFORM ENCEPHALOPATHY (BSE), TRANSMISSIBLE MINK ENCEPHALOPATHY (TME), ETC.
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                                                                                           Brain;
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                                                                                                                                                 IPR000817; Prion.
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REMOVED IN MATURE FORM (BY SIMILARITY).
GPI-ANCHOR (BY SIMILARITY).
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           BY SIMILARITY,
N-LINKED (GLC)
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Catarrhini;
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                        der Kuyl A.C., Dekker J.T., Goudsmit J.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: THE FUNCTION OF PAPP IS NOT KNOWN. PRP IS ENCODED IN THE
HOST GENOME AND IS EXPRESSED BOTH IN NORMAL AND INFECTED CELLS.
                                                                                                                                   Pfam; PF00377; prion; SMART; SM00157; PRP; 1
                                                                                                                                                                                                            modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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HSSP; P04925;
                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                           the European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                      (GSS), SCRAPIE, BOVINE SPONGIFORM ENCEPHALOPATHY (BSE), TRANSMISSIBLE MINK ENCEPHALOPATHY (TME), ETC. SIMILARITY: BELONGS TO THE PRION FAMILY.
                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor. DISEASE: PRP IS FOUND IN HIGH QUANTITY IN THE BRAIN OF HUMANS A ANIMALS INFECTED WITH THE DESCHERATIVE HEUROLOGICAL DISEASES KU CREUTZFELDT-JAKOB DISEASE (CJD), GERSTMANN-STRAUSSLER SYNDROME
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S X 8 AA TANDEM REPEATS (C
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OF P-H-G-G-G-W-G-
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HSSP; P04925; IAG2.
InterPro; IPR000817; Prion.
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SMART; SM00157; PRP; 1.
PROSITE; PS00291; PRION_1; 1.
PROSITE; PS00706; PRION_2; 1.
                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Submitted (NOV-1996) to the EM
-1- FUNCTION: THE FUNCTION OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
FUNCTION: THE FUNCTION OF PRP IS NOT KNOWN. PRP IS ENCODED IN THE HOST GENOME AND IS EXPRESSED BOTH IN NORMAL AND INFECTED CELLS.
SUBUNIT: PRP HAS A TENDENCY TO AGGREGATE YIELDING POLYMERS CALLED
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protein precursor (PrP) (PrP27-30) (PrP33-35C) (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Red-crowned mangabey) (Sooty mangabey)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MW.
 MAJOR PRION PROTEIN.

REMOVED IN MATURE FORM (BY SIMILARITY GPI-ANCHOR (BY SIMILARITY).

BY SIMILARITY.

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

S X 8 AA TANDEM REPEATS OF P-H-G-G-G-G-G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Goudsmit J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                       GPI-anchor; Repeat;
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                                                                                                              BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 55; DB 1; Pred. No. 0.042;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  D35D105BBEC53108 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vertebrata;
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                                                                                                                                    Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Euteleostomi;
                                                                                                                                                                                                                                                                                                                restrictions
                   P-H-G-G-G-W-G-
                                                                                  SIMILARITY).
                                                                                                                                                                                                                                                                                                                              EMBL
                                                                                                                                                                                                                                                                                                                                         a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                              outstation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIO_ATEPA
P51446;
01-OCT-1996
01-OCT-1996
01-OCT-1996
 LIPID
DISULFID
CARBOHYD
                                                                    Prion;
SIGNAL
                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                      "Infectious amyloid precursor gene sequences in primates used for experimental transmission of human spongiform encephalopathy."; Proc. Natl. Acad. Sci. U.S.A. 91:12159-12162(1994).
-i- FUNCTION: THE FUNCTION OF PRP IS NOT KNOWN, PRP IS ENCODED IN THE HOST GENOME AND IS EXPRESSED BOTH IN NORMAL AND INFECTED CELLS.
-i- SUBUNIT: PRP HAS A TENDENCY TO AGGREGATE YIELDING POLYMERS CALLED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REPEAT
REPEAT
REPEAT
REPEAT
REPEAT
                                                                                                                                                              EMBL; U15164; AAA68634.1; -
HSSP; P04156; 1E1G.
InterPro; IPR000817; Prion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Platyrrhini; Cebidae;
                                         PROPEP
                                                                                                                                     Pfam; PF00377; prion; 1 PRINTS; PR00341; PRION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cervenakova L., Brown P., Goldfarb L.G., Nagle J.,
Rubenstein R., Dubnick M., Gibbs C.J., Gajdusek D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Major prion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                        CHAIN
                                                                                              PROSITE;
                                                                                                           PROSITE;
                                                                                                                         SMART; SM00157; PRP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-95083661; PubMed-7991600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ateles paniscus (Black spider
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rissuE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49
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                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor. DISEASE: PRP IS FOUND IN HIGH QUANTITY IN THE BRAIN OF HUMANS ANIMALS INFECTED WITH THE DEGENERATIVE NEUROLOGICAL DISEASES KUCKEUTZFELDT-CAKOB DISEASE (CJD), GERSTMANN-STRAUSSLER SYNDROME (GSS), SCRAPIE, BOVINE SPONGIFORM ENCEPHALOPATHY (BSE),
                                                                                                                                                                                                                                                                                                                             TRANSMISSIBLE MINK ENCEPHALOPATHY (TME), ETC. SIMILARITY: BELONGS TO THE PRION FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GWGQPHGG 56
                                                                                  Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
8; Conser
                                                                                              PS00706; PRION_2;
                                                                                                           PS00291; PRION_1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Rel. 34, Created)
(Rel. 34, Last sequence update)
(Rel. 34, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein
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 ; Glycoprotein;
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230 252
230 252
239 252
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178 213
180 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       precursor
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68
76
84
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                                                                    GPI-anchor; Re
BY SIMILARITY
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MAJOR PRION PROTEIN.
REMOVED IN MATURE FORM (BY SIMILARITY).
GPI-ANCHOR (BY SIMILARITY).
BY SIMILARITY
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            monkey).
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0.042;
                                                                                Repeat;
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                                                                                Signal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pettrone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Euteleostomi;
Atelinae; Ateles.
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Best Local
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                                                                                                                                                                            EMBL; U08304; AAC50092.1; -. HSSP; P04925; 1AG2.
InterPro; IPR000817; Prion.
Pfam; PF00377; Prion; 1.
PRINTS; PR00341; PRION.
CMARTS; PR00341; PRION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            '_CALJA
PRIO_CALJA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P40247;
01-FEB-1995
01-FEB-1995
01-OCT-1996
  PROPEP
LIPID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

MEDLINE-95139066; PubMed-7837269;
MEDLINE-95139066; PubMed-7837269;
MEDLINE-95139066; PubMed-7837269;
MEDLINE-95139066; PubMed-7837269;
MEDLINE-9513906; PubMed-7837269;
MEDLINE-9513906; PubMed-7837269;
MEDLINE-9513906; PubMed-7837269;
MEDLINE-9513906; PubMed-7837269;
MEDLINE-95139066; PubMed
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REPEAT
                                                                                                                                                                                                                                                                                                                                                                                       the
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                                                                CHAIN
                                                                                   SIGNAL
                                                                                                       Prion;
                                                                                                                        PROSITE; PS00291; PRION_1; PROSITE; PS00706; PRION_2;
                                                                                                                                                                 SMART;
                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                         modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                use
                                                                                                                                                                                                                                                                                                                                                                                                        between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Callithrix jacchus (Common marmoset)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Major prion
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                                                                                                                                                                                                                                                                                                                                                                                 European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GSS), SCRAPIE, BOVINE SPONGIFORM ENCEPHALOPATHY (BSE), TRANSMISSIBLE MINK ENCEPHALOPATHY (TME), ETC. SIMILARITY: BELONGS TO THE PRION FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor. DISEASE: PRP IS FOUND IN HIGH QUANTITY IN THE BRAIN OF HUMANS AND ANIMALS INFECTED WITH THE DEGENERATIVE NEUROLOGICAL DISEASES KURU. CREUTZFELDT-JAKOB DISEASE (CJD), GERSTMANN-STRAUSSLER SYNDROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBUNIT: PRP HAS A TENDENCY TO "RODS".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOI. B101. 245:362-374(1995).
FUNCTION: THE FUNCTION OF PRP IS NOT KNOWN. PRP IS ENCODED IN THE HOST GENOME AND IS EXPRESSED BOTH IN NORMAL AND INFECTED CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GWGQPHGG
                                                                                                   Brain;
                                                                                                                                                               SM00157; PRP; 1
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8; Conser
                                                                                                                                                                                                                                                                                                                                                              non-profit
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(Rel.
(Rel.
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: Glycoprotein;
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178 213
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34,
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90
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4, Last annotation update)
precursor (PrP) (PrP27-30)
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66 2
74 3
82 4
90 5
27718 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chordata; Craniata; Vertebrata; Eutele
Primates; Platyrrhini; Callitrichidae;
                                                                                                                                                                                                                                                                                                                                                              institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
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GPI-anchor; Repeat; Signal.
BY SIMILARITY.
MAJOR PRION PROTEIN.
REMOVED IN MATURE FORM (BY SIMILARITY).
GPI-ANCHOR (BY SIMILARITY).
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                       agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-LINKED (GLCNAC. . .) (POTENTIAL).

5 X 8 AA TANDEM REPEATS OF P-H-G-G-W-G-
Q.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20EA38A42DCC56D1 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGGREGATE YIELDING POLYMERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cohen F.E.,
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Best Local
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01-FEB-1995
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SEQUENCE
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REPEAT
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LIPID
                                    CHAIN
                                                                                                  PRINTS; PR00341; PRION. SMART; SM00157; PRP; 1.
                                                                                                                       InterPro; IPR000817; Prion. Pfam; PF00377; prion; 1.
                                                                                                                                                                                                                                                                                                                                                                                   "Prion protein gene variation among primates.";

J. MOL. Biol. 245:362-374(1955).

-i- FUNCTION: THE FUNCTION OF PRP IS NOT KNOWN. PRP IS HOST GENOME AND IS EXPRESSED BOTH IN NORMAL AND IN HOST GENOME AND IS EXPRESSED BOTH IN NORMAL AND IN TROBUNT: PRP HAS A TENDENCY TO AGGREGATE VIELDING
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Mammalia; Eutheria; Primates; Platyrrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cebus apella (Brown-capped capuchin)
Eukaryota; Metazoa; Chordata; Crania
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 DISULFID
                                                  SIGNAL
                                                              Prion;
                                                                     PROSITE; PS00291; PRION_1; 1. PROSITE; PS00706; PRION_2; 1.
                                                                                                                                                EMBL; U08295; AAC50084.1; -. HSSP; P04156; 1E1G.
                                                                                                                                                                                      or send an
                                                                                                                                                                                                   entities
                                                                                                                                                                                                            modified and this statement is not removed.
                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ew the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor. DISEASE: PRP IS FOUND IN HIGH QUANTITY IN THE BRAIN OF HUMANS AND ANIMALS INFECTED WITH THE DECEMERATIVE NEUROLOGICAL DISEASES KURU. CREUTZFELDT-JAKOB DISEASE (CJD), GERSTMANN-STRAUSSLER SYNDROME
                                                                                                                                                                                                                                                                                   (GSS), SCRAPIE, BOVINE SPONGIFORM ENCEPHALOPATHY TRANSMISSIBLE MINK ENCEPHALOPATHY (TME), ETC. SIMILARITY: BELONGS TO THE PRION FAMILY.
                                                            Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
8; Conserv
                                                                                                                                                                                   requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
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252
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(Rel. 31, Last sequence update)
(Rel. 34, Last annotation update)
protein precursor (PrP) (PrP27-30) (PrP33-35C).
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BY SIMILARITY.

MAJOR PRION PROTEIN.

REMOVED IN MATURE FORM (BY SIMILARITY).

GPI-ANCHOR (BY SIMILARITY).

BY SIMILARITY.
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N-LINKED (GLCNAC. . .) (POTENTIAL).
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Pred. No. 0.043;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Platyrrhini; Cebidae;
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O_RABIT
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Q95211;
01-NOV-1997
CARBOHYD
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                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Species with apparent resistance to infection by prions.";
Gene 184:215-219(1997).
-I- FUNCTION: THE FUNCTION OF PRP IS NOT KNOWN. PRP IS ENCODED IN THE
HOST GENOME AND IS EXPRESSED BOTH IN NORMAL AND INFECTED CELLS.
-I- SUBBURIT: PRP HAS A TENDENCY TO AGGREGATE YIELDING POLYMERS CALLED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Major prion protein precursor (PrP) (PrP27-30) PRNP OR PRP.
                                              CHAIN
                                                                 SIGNAL
                                                                                           Prion; Brain;
                                                                                                                     PROSITE; PS00291; PRION_1; PROSITE; PS00706; PRION_2;
                                                                                                                                                                                           Pfam; PF00377; prion; 1. PRINTS; PR00341; PRION.
                                                                                                                                                                                                                                                                  EMBL; U28334; AAC48697.1; -. HSSP; P10279; 1DWY.
                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=New Zealand white; MEDLINE=97183665; PubMed=9031631;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Characterization of a prion protein (PrP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Coftus B., Rogers M.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISEASE: PRP IS FOUND IN HIGH QUANTITY IN THE BRAIN OF HUMANS ANIMALS INFECTED WITH THE DEGENERATIVE NEUROLOGICAL DISEASES KI CREUTZFELDT-JAKOB DISEASE (CJD), GERSTMANN-STRAUSSLER SYNDROME (GSS), SCRAPIE, BOVINE SPONGIFORM ENCEPHALOPATHY (BSE), TRANSMISSIBLE MINK ENCEPHALODATHY (THE PROPERTY OF THE PROPERTY OF TRANSMISSIBLE MINK ENCEPHALODATHY (THE PROPERTY OF THE PROPERTY OF 
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N-LINKED (GLCNAC. . .) (POTENTIAL).
5 X 8 AA TANDEM REPEATS OF P-H-G-G-G-Q.
1.
               N-LINKED (GLCNAC. . .) (POTENTIAL)
                                       MAJOR PRION PROTEIN.
                                                                   POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 55; DB 1;
Pred. No. 0.043;
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PRIO_COLGU
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Best Local
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                                                                         EMBL; U08297;
EMBL; U75389;
HSSP; P04925;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1995
01-FEB-1995
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 8-253 FROM N.A.

der Kuyl A.C., Dekker J.T., Goudsmit J.;

Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.

Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.

FUNCTION: THE FUNCTION OF PRP IS NOT KNOWN. PRP IS ENCODED IN THE HOST GENOME AND IS EXPRESSED BOTH IN NORMAL AND INFECTED CELLS.

-!- SUBUNIT: PRP HAS A TENDENCY TO AGGREGATE YIELDING POLYMERS CALLED
                                                                                                                                                                                                                                                                       This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schatzl H.M., Dacosta M., Taylor L., Cohen F.E. "Prion protein gene variation among primates."; J. Mol. Biol. 245:362-374(1995).
Pfam; PF00377; prion; 1
PRINTS; PR00341; PRION.
SMART; SM00157; PRP; 1.
                                                                                                                                                      entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                         use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIO_COLGU
P40251;
                                                                                                                                                                                                                             the European Bioinformatics Institute.
                                                                                                                                                                                                                                                     between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=95139066; PubMed=7837269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Colobus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Colobus guereza (Black-and-white colobus monkey)
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                                                         InterPro;
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                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Attached to the membrane by a GPT anchor. DISEASE: PRP IS FOUND IN HIGH QUANTITY IN THE BRAIN OF HUMANS AND ANIMALS INFECTED WITH THE DECEMERATIVE NEUROLOGICAL DISEASES KURU CREUTZFELDT-JAKOB DISEASE (CJD), GERSTMANN-STRAUSSLER SYNDROME
                                                                                                                                                                                                                                                                                                        SIMILARITY: BELONGS TO THE PRION FAMILY.
                                                                                                                                                                                                                                                                                                                          (GSS), SCRAPIE, BOVINE SPONGIFORM ENCEPHALOPATHY (BSE), TRANSMISSIBLE MINK ENCEPHALOPATHY (TME), ETC.
                                                                                                                                                                                                                                               SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation
                                                       IPR000817; Prion
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(Rel. 31, Last sequence update)
(Rel. 40, Last annotation update)
protein precursor (PrP) (PrP27-30)
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5 X 8 AA TANDEM REPEATS OF P-H-G-G-G-W-G-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 55; DB 1;
Pred. No. 0.043;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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                                                                                                                                                                                                       There are no restrictions ng as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AΑ
                                                                                                                                                                      http://www.isb-sib
                                                                                                                                                                                         Usage
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PROSITE; PROSITE;

PS00291;

PRION_1;

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Search completed: January 3, 2003, 15:29:18 Job time: 7.90909 secs
                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 55; DB 1; Length 253; Best Local Similarity 100.0%; Pred. No. 0.043; atches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Prion; Brain; OSIGNAL 2: CHAIN 2: PROPEP 23: LIPID 17: CARBOHYD 18: CARBOHYD 19: DOMAIN 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REPEAT
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                                                                                                                                                                       1 GWGQPHGG 8
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56 GWGQPHGG 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rain; Glycoprotein; GPI-anchor; Repeat; Signal.

1 22 BY SIMILARITY.

23 230 MAJOR PRION PROTEIN.

23 230 REMOVED IN MATURE FORM (BY SIMILARITY).

230 230 REMOVED IN MATURE FORM (BY SIMILARITY).

231 253 REMOVED IN MATURE FORM (BY SIMILARITY).

232 230 GPI-ANCHOR (BY SIMILARITY).

233 230 CPI-ANCHOR (BY SIMILARITY).

244 BY SIMILARITY.

257 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).

258 AN TANDEM REPEATS OF P-H-G-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G-W-G
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Result
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     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed.
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O97905 tursiops tr
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O97694 cervus nipp
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O97693 canis lupus
O97912 bison bonas
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homo	Q8TBG0	4	253	00.	55	41
Q96e70 homo sapien	Q96E70	4	253	00.	55	40
homo	Q9UP19	4	253	100.0	55	39
Q8vhv5 clethrionom	Q8VHV5	11	248	00.	55	38 8
O60489 homo sapien	060489	4	246	00.	55	37
Q9mzu7 odocoileus	Q9MZU7	6	245	00.	55	36
Q15216 homo sapien	Q15216	4	245	00.	55	35
5 mesocric	P97895	11	243	00.	55	34
	Q8VHV4	11	240	00.	55	33
097695 giraffa cam	097695	6	235	00.	55	32
	P78446	4	233	00.	55	31
_	097964	δ	227	00.	55	30
	097909	σ	227	00.	55	29
	097906	σ	227	00.	55	28
	097907	6	226	100.0	55	27
_	097910	σ	223		55	26
097913 equus quagg	097913	6	222	00.	55	25
odoc	002825	6	220	00.	55	24
bos	Q9TV00	6	216	00.	55	23
097904 bos javanic	097904	σ	215	00.	55	22
canis	Q9TV03	σ	214	00.	55	21
	Q9TV04	σ	213	100.0	55	20
097698 cervus elap	097698	σ	212	00.	ري در	19
7787	077787	σ	211	100.0	55	18
Q9tv02 camelus dro	Q9TV02	σ	209	100.0	55	17

ALIGNMENTS

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Q16409
Q16409; Q16407;
Q1-NOV-1996 (Tri
01-NOV-1996 (Tri
01-JUN-2002 (Tri
                                                                                                                                                           SEQUENCE OF 1-89 FROM N.A.
MEDLINE-96057178; PubMed=7572084;
Oda T., Kitamoto T., Tateishi J., Mitsuhashi
Oguni E., kato Y., Tominaga I., Yanai K.;
"Prion disease with 144 base pair insertion i
line.";
Cochran E.J., Bennett D.A., Cervenakova L., Kenney K., Bernard B., Foster N.L., Benson D.F., Goldfarb L.G., Brown P.; "Familial Creutzfeldt-Jakob disease with a five-repeat octapeptide insert mutation."; Neurology 47:727-733(1996).
EMBL; S80539, AAB213441; -.
EMBL; S79978; AAB35416.1; -.
                                                                                                                                                                                                                                                                  MEDLINE-92140671; PubMed=1736177;
Brown P., Goldfarb L. G., McCombie W.R., Nieto A., Squillacote D.
Sheremata W., Little B.W., Godec M.S., Gibbs C.J. Jr., Gajdusek
"Atypical Creutzfeldt-Jakob disease in an American family with a
"nsert mutation in the PRNP amyloid precursor gene.";
                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                  SEQUENCE OF 1-81 FROM N.A. MEDLINE=96390485; PubMed=8797471;
                                                                                                                               Acta Neuropathol. [3]
                                                                                                                                                                                                                                            Neurology 42:422-427(1992).
                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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(Fragment).
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Q9WUJ1;
01-NOV-1999
01-NOV-1999
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SEQUENCE
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J. Mol. Biol. 289:1163-1178(1999).
EMBL; AF113944; AAD13922.1;
Interpro; IPR002395; Kininogen.
Interpro; IPR000817; Prion.
                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-97317556; PubMed-9174569;
Schatzl H.M., Wopfner F., Gilch S., von Brunn
"Is codon 129 of prion protein polymorphic in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF0037/; pr
PRINTS; PR00341;
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PRINTS; PR00334; KININOGEN.
PRINTS; PR00341; PRION.
SMART; SM00157; PRP; 1.
                                                                                                                                                                                                                                                                                                       Wopfner F., Weidenhofer G., Schneider R., von Brunn A., Gilch
Schwarz T.F., Werner T., Schatzl H.M.;
"Analysis of 27 mammalian and 9 avian PrPs reveals high conser-
                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDILINE=99303687; PubMed=10373359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Muntiacus muntjak (Muntjak).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidea;
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InterPro; IPR000817; Prion.
Pfam; PF00377; prion; 2.
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                                                                                                                                                                                                                                                                                                                                        susceptible lemur monkey.";
Submitted (AUG-1999) to the
EMBL; AF177293; AAD54335.1;
                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
Gilch S., Schatzl H.M.;
"Unusual prion protein octarepeat structure of the highly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 *Expression of Prion Protein in Human Lenses.";

*Expression of Prion Protein in Human Lenses.";

Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF139166; AAD24491.1;

Interpro; IPR000817; Prion.
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Cavia porcellus (Guínea pig).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=OCULAR LENS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11818 MW;
                                                                 100.0%;
                                                                                                                                     13436 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                               EMBL/GenBank/DDBJ databases
                                       Score 55; DB 6
Pred. No. 0.1;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 55;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi;
Hystricognathi; Caviidae; Cavia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strepsirhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                     CC2C8A5A855A7C94 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               124
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                                                                                      6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lemuridae; Varecia.
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                                              Indels
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  Query Match
Best Local S
Matches 8
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Ovis aries (Sheep).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9MZ17;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                      HSSP; P10279; 1DWY.
InterPro; IPRO08817; Prion.
Pfam; PF00377; prion; 1.
PRINTS; PR00341; PRION.
SMART; SM00157; PRP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NON_TER
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of the prion protein.";

J. Mol. Biol. 289:1163-1178(1999).
                                                                                                                                                                                                                                     susceptible sheep.";
Submitted (MAY-2000) to the
Submitted (MAY-2000) to the
EMBL; AF267507; AAF91403.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9MZ17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00377; prion; 1. PRINTS; PR00341; PRION. SMART; SM00157; PRP; 1.
                                                                                                 PROSITE; PS00291; PRION_1; 1.
                                                                                                                                                                                                                                                                                                                        Knowles D.P.;
                                                                                                                                                                                                                                                                                                                                          Herrmann
                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                Bovidae; Caprinae; Ovis.
NCBI_TaxID=9940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Prion protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP; P10279; 1DWY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF117311; AAD19982.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=99303687; PubMed=10373359;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tursiops
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tursiops truncatus (Atlantic bottle-nosed dolphin). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Prion protein (Fragment).
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01-JUN-2002
                                                                                                                                                                                                                                                                                             "Detection of PrPc in peripheral blood mononuclear cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9739;
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  Similarity
8; Conserv
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8; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PS00291; PRION_1;
                                                                                                                                                                                                                                                                                                                                        L.M., Davis W.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPR000817; Prion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               141 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TrEMBLrel. 10, Last sequence update) (TrEMBLrel. 21, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TrEMBLrel.
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43
                                                                              AA;
                                                                                14428 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15066 MW;
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                  100.0%;
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                                                                                                                                                                                                                                                                                                                                        Η.,
                  Score 55; DB 6
Pred. No. 0.12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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Pred. No. 0.12;
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  Mismatches
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                                     DB 6; Length 143;
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  0;
  Indels
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                                                                                                                                                                                                                                                                                                                                        Gambetti P.
                                                                                                                                                                                                                                                                                                 of scrapie
0;
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Gaps
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097911
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RESULT 8
097694
Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      097911;
                                                                                                                                                                                                      01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10, 01-JUN-2002 (TrEMBLrel. 21,
                                    "Is codon 129 animals?";
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                                                              Schatzl H.M.,
                                                                        SEQUENCE FROM N.A. MEDLINE=97317556; PubMed=9174569;
                                                                                                                            Mammalia; Eutheria;
Cervidae; Cervinae;
                                                                                                                                                    Eukaryota;
                                                                                                                                                                  Cervus nippon dybowskii
                                                                                                                                                                                           Prion protein
                                                                                                                                                                                                                                             097694;
                                                                                                                                                                                                                                                           097694
                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00377; prion; 1.
PRINTS; PR00334; KININOGEN.
PRINTS; PR00341; PRION.
SMART; SM00157; PRP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002395; Kininogen.
InterPro; IPR000817; Prion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF117326; AAD19997.1; -. HSSP; P10279; 1DWY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=PBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bovidae; Caprinae; Budorcas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Budorcas taxicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Prion protein
SEQUENCE FROM N.A
                        Lancet 349:1603-1604(1997)
                                                                                                                NCBI_TaxID=88066;
                                                                                                                                                                                                                                                                                                                                                                                                                                             NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                        NON_TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=99303687; PubMed=10373359;
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                                                                                                                                                                                                                                                                                                                                                                                          Local
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8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                              181
181 AA;
                                                                                                                          Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoide
Cervinae; Cervus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Metazoa;
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                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                               of prion protein polymorphic
                                                              Wopfner F.,
                                                                                                                                                                                           (Fragment).
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; Chordata;
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                                                                                                                                                                                                                                                                                                                                                                                                                              19253 MW;
                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
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10,
21,
                                                              Gilch S.,
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Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                        Score 55; DB 6
Pred. No. 0.15;
                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                              A9001D086442E92A CRC64;
                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence update)
                                               von Brunn
morphic in
                                                                                                                                                                                                                                                           185
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                                                A., Ja
human
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                                                                                                                                                                                                                                                                                                                                                                                                     Length 181;
                                                            Jager G.;
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                                                beings but not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gilch
                                                                                                                                         Cervoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bovoidea;
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InterPro; IPR000817; Prion.
Pfam; PP00377; Prion; 1.
PRINTS; PR00334; KININOGEN.
PRINTS; PR00341; PRION.
SMART; SM00157; PRP; 1.
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SEQUENCE
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"Analysis of 27 mammalian and 9 avian PrPs reveals high conservation of flexible regions of the prion protein.";
J. Mol. Biol. 289:1163-1178(1999).
EMBL; AF117309; AAD19980.1; -.
HSSP; P10279; IDWY.
InterPro; IPR002395; Kininogen.
InterPro; IPR002395; Kininogen.
InterPro; IPR00334; KININOGEN.
PRINTS; PR00334; KININOGEN.
PRINTS; PR00341; PRION.
SMART; SM00157; PRP; 1.
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"Analysis of 27 mammalian and 9 avian PrPs reveals high conservation of flexible regions of the prion protein.";
J. Mol. Biol. 289:1163-1178(1999).
EMBL; AF113941; AAD13289.1;
HSSP: P10279; IDWY.
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NCBI_TaxID=59515;
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Mammalla; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Addax nasomaculatus
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                                 GWGQPHGG 8
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llarity 100.0%;
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Pred. No. 0.16;
Mismatches
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Pred. No. 0.16;
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EMBL; AF117328; AAD19999.1;
HSSP; P10279; 1DWY.
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097693;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
Bovidae; Bovinae; Bison.
NCBI_TaxID=9902;
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J. Mol. Biol. 289:1163-1178(1999).
EMBL; AF113939; AAD12063.1; -.
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                                                                                                                                                                                                                                          Schwarz T.F., Werner T., Schatzl H.M.;

"Analysis of 27 mammalian and 9 avian PrPs reveals high conservation of flexible regions of the prion protein.";

J. Mol. Biol. 289:1163-1178(1999).
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PRINTS; PR00341; PRION.
SMART; SM00157; PRP; 1.
PROSITE; PS00291; PRION_1;
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                                                               InterPro; IPR001610; PAC. InterPro; IPR000817; Prion.
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                             Pfam; PF00377; prion;
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Pred. No. 0.16;
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                                                                                                                                                                                                                                                                                                                                                                                           von Brunn A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 195;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                           Gilch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
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PRINTS;

PR00334;

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RESULT 13
097696
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     GR DOT AC
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                                                                                                                                                                                                                                                                                                                                                                                                          RA Wopfner F., Weidenhofer G., Schneider R., von Brunn A., Gilch S.,

Schwarz T.F., Werner T., Schatzl H.M.;

"Analysis of 27 mammalian and 9 avian PrPs reveals high conservation

RT of flexible regions of the prion protein.";

J. Mol. Biol. 289:1163-1178(1999).

BR J. Marian Protein. ";

BR L. J. Marian Protein.";

BR L. J. Marian Protein. ";

BR HSSP; P10279; 1DWY.

BR InterPro; IPR000817; Prion.

BR InterPro; IPR002395; Kininogen.

BR InterPro; IPR002395; Kininogen.

BR InterPro; IPR002395; Kininogen.

BR PRINTS; PR00377; Prion; 1.

BR PRINTS; PR00334; KININOGEN.

SMART; SM00157; PRFON.

PROSITE; PS00291; PRION.1; 1.

PROSITE; PS00706; PRION.1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 12
                                                                                                                                                                                                                                                                                                      Query Match
Best Local :
                                                                                                                                                                                                                                                                                     Matches
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Best Local :
               097696 PRELIMINARY;
097696;
01-MAY-1999 (TrEMBLrel. 10, C
01-MAY-1999 (TrEMBLrel. 10, L
01-JUN-2002 (TrEMBLrel. 21, L
Prion protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00086; PAC; 1.
SMART; SM00157; PRF; 1.
PROSITE; PS00291; PRION_1; 1.
PROSITE; PS00706; PRION_2; 1.
NON_TER 1 1
NON_TER 200 200
SEQUENCE 200 AA; 21674 MW;
                                                                                                                                                                                                                                                                                                                                                             NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                PROSITE;
PROSITE;
NON_TER
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097908;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Capra nubiana (Nubian ibex).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-1999 (TrEMBLrel. 10,
01-MAY-1999 (TrEMBLrel. 10,
01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=99303687; PubMed=10373359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-PBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=72543;
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                                                                                                                                                                                                            31 GWGQPHGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16 GWGQPHGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                            1 GWGQPHGG
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                                                                                                                                                                                                                                                                                 Similarity
8; Conserv
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8; Conser
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                                                                                                                                                                                                                                                                                                                                                           202
202 AA;
                                                                                                                                                                                                                                                                                 100.0%; ilarity 100.0%; Conservative 0
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                                                                                                                                                                                                            38
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                                                                                                                                                                                                                                                                                                                                                             21949 MW;
                                 Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                     0;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                 Score 55; DB
Pred. No. 0.1
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 55; DB 6
Pred. No. 0.17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                             DB0634A43B4DB77F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1F270CDF4BE5271B CRC64;
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                                                                                                                 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      202
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                                                                                                                                                                                                                                                                                   0;
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                                                                                                                                                                                                                                                                                                                    Length 202;
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                                                                                                                                                                                                                                                                                   0;
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097629
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NON_TER
SEQUENCE
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NON_TER
SEQUENCE
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 1 GWGQPHGG
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Query Match
Best Local Similarity
Matches 8; Conserv
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Best Local Similarity
Matches 8; Conser
                                                                                                                                                        InterPro; IPR002395; Kininogen.
InterPro; IPR000817; Prion.
Pfam; PP00377; Prion; 1.
PRINTS; PR00334; KININOGEN.
PRINTS; PR00341; PRION.
SMART; SM00157; PRP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  097629 PRELIMINARY;
097629;
01-MAY-1999 (TrEMBLrel. 10,
01-MAY-1999 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                TISSUE-BRAIN;
O'Rourke K.I., Miller M.W., Wild
O'rourke in free ranging and
                                                                                                                                                                                                                                                                Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases EMBL; AF091558; AAC69626.1; -. HSSP; P10279; 1DWY.
                                                                                                                                                                                                                                                                                                                     "PrP alleles in free ranging virginianus).";
                                                                                                                                                                                                                                                                                                                                                                                                                                             Odocoileus virginianus (white-tailed deer).
Eukaryota; Metazoa; Chordata; Cranitata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoide
Cervidae; Odocoileinae; Odocoileus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000817; Prion.
pfam; pF00377; prion; 1.
pRINTS; PR00341; pRION.
SMART; SM00157; PRP; 1.
pROSITE; PS00291; PRION_1;
                                                                                                                                                                                                                                                                                                                                                                                                               Prion protein (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wopfner F., Weidenhofer G., Schmeider R., von Brunn
Schwarz T.F., Werner T., Schatzl H.M.;
"Analysis of 27 mammalian and 9 avian PrPs reveals
                                                                                                                       PROSITE; PS00291; PRION_1; 1. PROSITE; PS00706; PRION_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00291; PRION_1; PROSITE; PS00706; PRION_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE=99303687; PubMed=10373359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9844;
[1]
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Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Lama.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lama glama (Llama).
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       flexible regions of the prion protein.", Mol. Biol. 289:1163-1178(1999).
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202 AA;
                                                                      204
204 AA;
 Conservative
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                                                                      204
22154 MW;
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21860 MW;
              100.0%;
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Last annotation updat
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Score 55; DB 6
Pred. No. 0.17;
Mismatches
                                                                       CA8AE68F2B49C81E CRC64;
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                                                                                                                                                                                                                                                                                                                                      M.A., Williams captive white
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                                                                                                                                                                                                                                                                                                                                      s E.S.;
tailed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 202;
                                 Length 204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pecora; Cervoidea;
 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                        deer
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0;
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 Gaps
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0;
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Search completed: January 3, 2003, 15:31:54
                                                                                                                               Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                  Odocoileus virginianus (white-tailed deer).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidea;
Cervidae; Odocoileinae; Odocoileus.
NCBI_TaxID=9874;
                                                                                                           NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                               O9TSI8 PRELIMINARY: PRT; 204 AA.
O9TSI8:
O1-MAY-2000 (TrEMBLrel. 13, Created)
O1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
O1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Prion protein (Fragment).
                                     36 GWGQPHGG 43
                                                                                                                                                                                                                                                                                                                                                                                                                          11111111
36 GWGQPHGG 43
                                              1 GWGQPHGG 8
                                                                                                           204 :
204 AA;
                                                                      100.0%; Score 55; DB 6; Length 204; ilarity 100.0%; Pred. No. 0.17; Conservative 0; Mismatches 0; Indels
                                                                                                204
22181 MW; CA962B93FA84D4D3 CRC64;
                                                                       0,
                                                                       Gaps
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Sequence Sequence

7, Appli 26, Appl 28, Appl 28, Appl 1, Appli 19, Appli 28, Appli 28, Appli 4, Appli 5, Appli 6, Appli 7, Appli 7, Appli 7, Appli 8, Appli 9, Appli 9, Appli 9, Appli 10, Appli 11, Appli 12, Appli 12, Appli 12, Appli 13, Appli 14, Appli 16, Appli 17, Appli 18, Appli 19, App

Sequence Sequence Sequence Sequence

Sequence

Sequence Sequence Sequence

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Sequence

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Result
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Run on:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          l number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                        Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Issued_Patents_AA:*
1: /cgn2_6/ptodata/1,
2: /cgn2_6/ptodata/1,
3: /cgn2_6/ptodata/1,
4: /cgn2_6/ptodata/1,
5: /cgn2_6/ptodata/1,
6: /cgn2_6/ptodata/1,
                                                                                                                                                                                                                                                                                                                                                                        Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-543-188A-1
55
    January 3, 2003, 15:25:16; Search time 12 Seconds (without alignments)
19.615 Million cell updates/sec
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Listing first 45 summaries
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
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/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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US-08-244-701B-37
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US-09-076-721-27
US-09-076-721-36
US-09-076-721-37
US-09-076-721-36
US-09-18-450-18
US-09-18-450-18
US-09-18-450-18
US-09-18-450-18
US-08-60-626-8
US-08-660-626-8
US-08-660-626-8
US-08-692-892-2
US-08-692-892-2
US-08-692-892-2
US-08-692-892-2
US-09-128-450-20
US-08-242-188-1
US-08-660-626-7
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US-08-244-701B-24
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; Patent No.
; GENERAL IN
                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/244,701B
FILING DATE: 02-UUN-1994
CLASSIFETCATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Fanucci, Allan A.
REGISTRATION NUMBER: 30,256
REFERENCE/DOCKET NUMBER: 8080-007
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                   TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Fishleigh, Robert V.
APPLICANT: Robson, Barry
APPLICANT: Mee, Roger P.
TITLE OF INVENTION: Fragments of Prion Proteins
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
                        LOCATION: 1
OTHER INFORMATION: /label= X
OTHER INFORMATION: /note= "X may be
OTHER INFORMATION: of Y and denotes
FEATURE:
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                                                                                                         FEATURE:
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 NAME/KEY:
LOCATION:
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ZIP: 10036
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STATE: New Yorl
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                                                                                           NAME/KEY:
                                                                                                                                          STRANDEDNESS:
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o. 5773572
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US-09-128-450-28
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US-09-128-450-28
US-09-823-494-28
US-09-823-494-28
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US-08-600-626-10
US-08-600-626-10
US-08-713-939A-4
US-08-868-162A-24
US-09-031-168A-24
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US-09-031-165A-24
US-09-031-165A-24
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Version

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one or more amino

independently acid(s)"

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; OTHER INFORMATION:
; OTHER INFORMATION:
US-08-244-7018-24
 Query Match
Best Local Similarity
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; OTHER INFORMATION:
; OTHER INFORMATION:
US-08-244-701B-27
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US-08-244-701B-27
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Best Local :
                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (212) /90-2007
TELEPAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
TELEX: 66141 PENNIE
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Fanucci, Allan A.
REGISTRATION NUMBER: 30,256
REFERENCE/DOCKET NUMBER: 808
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 212) 790-9090
TELECOMMUNICATION 2120 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION: NAME: Fanucci, Allan A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                           OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                            NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                          TOPOLOGY: 11
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Similarity 100.0%;
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Mee, Roger P.
WENTION: Fragments of Prion Proteins
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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             100.0%; Score 55; DB 1; 100.0%; Pred. No. 0.017; tive 0; Mismatches
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/note= "Y may be absent or present independently
of X and denotes one or more amino acid(s)"
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/note= "Y may be absent or present independently
of X and denotes one or more amino acid(s)"
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Pred. No. 0.(
0; Mismatches
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0.017;
                                              DB 1; Length 18;
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RESULT 4
US-09-076-721-24
; Sequence 24, Application US/09076721
; Patent No. 6379905
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                                                                                                                                                             Matches
                                                                                                                                                                                           Query Match
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT: Robson, E
APPLICANT: Mee, Roge
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/244,701B
FILING DATE: 02-70N-1994
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Fanucci, Allan A. REGERATION NUMBER: 30,256
REFERENCE/DOCKET NUMBER: 80
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                         OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ZIP: 10036
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1155 Avenue of the Americas
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(212) 869-8864/9741
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                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                         /label= Y
/note= "Y may be absent or present independently
of X and denotes one or more amino acid(s)"
                                                                                                                                                                                                                                                                                                                                      /label= X
/note= "X is absent or present independently of Y
and denotes one or more amino acid(s)"
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                                                                                                                                                                          Score 55; DB 1;
Pred. No. 0.017;
                                                                                                                                                             Mismatches
                                                                                                                                                                                           DB 1; Length 18;
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Indels

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Gaps

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GENERAL INFORMATION:

APPLICANT:

APPLICANT:

Robson,

Barry

Fishleigh, Robert V.

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RESULT 5
US-09-076-721-27
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                                                                                                                                                                                                                                                                                                                                 US-09-076-721-24
Sequence 27, Application US/09076721
Patent No. 6379905
GENERAL INFORMATION:
APPLICANT: Fishleigh, Robert V.
APPLICANT: Robson, Barry
APPLICANT: Mee, Roger P.
TITLE OF INVENTION: Fragments of Prion Proteins
NUMBER OF SEQUENCES: 67
                                                                                                                                                                                                                                                                                   Query Match
Best Local :
                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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APPLICATION NUMBER:
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OTHER INFORMATION:
OTHER INFORMATION:
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4 GWGQPHGG 11
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OTHER INFORMATION:
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REGISTRATION NUMBER: 30,256
REFERENCE/DOCKET NUMBER: 80
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: Modified-site LOCATION: 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10036
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                                                                                                                                                                                                                                                                               100.0%;
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                                                                                                                                                                                                                                                                                                                                              /label= Y
/note= "Y may be
of X and denotes
                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= x
/note= "X may be absent or present independently
of Y and denotes one or more amino acid(s)"
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                                                                                                                                                                                                                                                                               Score 55; DB 4;
Pred. No. 0.017;
                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                              absent or present independently
one or more amino acid(s)"
                                                                                                                                                                                                                                                                                                DB 4;
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RESULT 6
US-09-076-721-30
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                                                                                                                                                                       Sequence 30, Application US/09076721 Patent No. 6379905 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 8; Conserv
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                                                                                                                           APPLICANT:
APPLICANT:
                                                                                                    TITLE OF INVENTION: Fraq
                                                                             CORRESPONDENCE ADDRESS:
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LENGTH: 18 amino acids
TYPE: amino acid
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
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ATTORNEY/AGENT INFORMATION:
NAME: Fanucci, Allan A.
REGISTRATION NUMBER: 30,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
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                                                                                               NUMBER OF SEQUENCES:
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OTHER INFORMATION: /note= "Y may be absent or present independently
OTHER INFORMATION: of X and denotes one or more amino acid(s)"
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LOCATION:
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 COUNTRY:
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                                                            ADDRESSEE:
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New York
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1155 Avenue of the Americas
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                                                                                                                                                       Fishleigh, Robert V.
                                                                                                                                          Robson, Barry
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                                                                                             Fragments of Prion Proteins 67
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/note= "X may be absent or present independently
of Y and denotes one or more amino acid(s)"
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INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Fragments of Prion Proteins NUMBER OF SEQUENCES: 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Fishleigh, Robert V. APPLICANT: Robson, Barry APPLICANT: Mee, Roger P. Transper, Roger P. Transpe
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
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LOCATION: 18
OTHER INFORMATION:
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                   STATE: New York
                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                        COUNTRY: UZIP: 10036
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OTHER INFORMATION: /note= "X is absent or present independently of Y
OTHER INFORMATION: and denotes one or more amino acid(s)"
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE:
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                                                                                                                                                                                                                            U.S.A.
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PatentIn Release #1.0, Version #1.25
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/note= "Y may be absent or present
of X and denotes one or more amino
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                                                     TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 02-JUN-19
                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 790-9090
                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Fragments of Prion Proteins NUMBER OF SEQUENCES: 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Fishleigh, RO
APPLICANT: Robson, Barry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 80 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Fanucci, Allan A.
REGISTRATION NUMBER: 30,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (212,
TELEFAX: 66141 PENNIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (212) /20 TELEPHONE: (212) 869-8864/9741
                                                                                                         TELEFAX:
                                                                                                                                                           REFERENCE/DOCKET NUMBER:
                                                                                                                                                                        NAME: Fanucci, Allan A. REGISTRATION NUMBER: 30,256
                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 1155 Avenue of the Americas CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE:
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               STRANDEDNESS:
                                              LENGTH:
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                            amino acid
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                                           26 amino acids
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                                                                                                          (212) 869-8864/9741
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linear
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                                                                                                                                                                                                                                                                                                                                                                                    Floppy disk
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                                                                                                                                                                                                                                         US 08/244,701
                                                                                                                                                                                                                                                                                                       US/09/076,721
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Pred. No. 0.024;
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; FEATURE:
; NAME/KEY: NON_TER
; LOCATION: (1)..(2)
US-09-823-494-18
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Best Local S
Matches 8
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CURRENT FILING DATE: 1998-08-03
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 18, Application US/09128450 Patent No. 6211149 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Chesebro, Bruce W
APPLICANT: Caughey, Byron W
APPLICANT: Chabry, Joelle
APPLICANT: Priola, Susette
TITLE OF INVENTION: Inhibitors of Formation of Protease Resistant Prion
FILE REFERENCE: 50121
CURRENT APPLICAMENT
                                                                                                               SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                         APPLICANT: Chabry, Joelle
APPLICANT: Priola, Susette
TITLE OF INVENTION: Inhibitors of Formation of Protease Resistant Prion
TITLE OF INVENTION: Protein
FILE REFERENCE: 50121
                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/823,494
CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/128,450
PRIOR FILING DATE: 1998-08-03
                                                                                                                                               NUMBER OF SEQ ID NOS: 29
                                                                                                                                                                                                                                                                                                        APPLICANT: Chesebro, Bruce W
APPLICANT: Caughey, Byron W
                                                                                                                                                                                                                                                                                                                                            ENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                             equence 18, Appli
atent No. 6355610
                                                       TYPE: PRT
ORGANISM: Hamster sp.
                                                                                                                                                                                                                                                                                                                                                                                           09-823-494-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 208
TYPE: PRT
ORGANISM: Hamster sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: NON_TER LOCATION: (1)..(2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                              LENGTH: 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                           34 GWGQPHGG 41
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nes 8; Conserv
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100.0%; Pred. No. 0.18;
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RESULT 12
US-08-509-261A-2
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Best Local Similarity
"~+~hes 8; Conserv
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                                                                     Sequence 2, Application US/08509261A Patent No. 5763244 GENERAL INFORMATION:
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Best Local Similarity
Matches 8; Conserv
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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                            APPLICANT:
APPLICANT:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/242,188
FILING DATE: 13-MAY-1994
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
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NAME: Bosicevic, Karl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS
 TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
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                                                                                                                                                                             56 GWGQPHGG
                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
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                                                                                                                                                                                                                                                                                                       ORGANISM: HUMAN PRION PROTEIN, HuPrP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                              253 amino acids
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2200 Sand Hill Road
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                            Telling, Glenn
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                                            Prusiner, Stanley B. Scott, Michael R.
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Method of Detecting Prions in a Sample and Transgenic
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Pred. No. 0.
                                                                                                                                                                                                                                   Mismatches
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   Animal Used fore
                                                                                                                                                                                                                                                              Length 253;
                                                                                                                                                                                                                                     Indels
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NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:

ADDRESSEE: Bozicevic & Reed, LLP STREET: 285 Hamilton Avenue, Suite 200 CITY: Palo Alto STATE: CA

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Best Local Similarity
Matches 8; Conserv
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atent No. 5789655
GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
                                                                                                                                                                                                                                                   APPLICANT: Fred E. Coher APPLICANT: Michael R. Sc
TITLE OF INVENTION: TRAI
TITLE OF INVENTION: EDITION: EDITION:
                                                  SOFTWARE: ASCIII
CURRENT APPLICATION DATA:
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TELECOMMUNICATION INFORMATION: 650-327-3400
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SOETWARE: PastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                       COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: BOZICEVIC, Karl
REGISTRATION NUMBER: 28,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 800 PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
COMPUTER: IBM Compat
                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Stanley B. Prusiner APPLICANT: Glenn C. Telling
                                                                                                                                                                                         STREET: 2200 Sand Hill Road, Suite 100 CITY: Menlo Park
STATE: California
                   APPLICATION NUMBER: US/08/660,626 FILING DATE:
                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56 GWGQPHGG 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: sir
CLASSIFICATION: 435
                                                                                                                   MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/01
FILING DATE: 31-JUL-1995
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                                                                                                                                                         94025
                                                                                                                                                                                                                                                                                                                         Glenn C. Telling
Fred E. Cohen
Michael R. Scott
                                                                                                                                                                         USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Diskette
IBM Compatible
                                                                                                                                                                                                                                             Fish & Richardson
                                                                                                                   Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 single
                                                                                                                                                                                                                                                                                            TRANSGENIC ANIMALS EXPRESSING EPITOPE-TAGGED PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 55; DB 1 100.0%; Pred. No. 0.22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US/08/509,261A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28,807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 253;
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US-08-692-892-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No. 579290
   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                          TELEFAX: (415) 854-U8 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (415) 854-0875 INFORMATION FOR SEQ ID NO: 8:
                                                              TOPOLOGY: lin
MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC COMPUTIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/692,892
                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Valeta Gregg
REGISTRATION NUMBER: 35,127
REFERENCE/DOCKET NUMBER: 07
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 322-5070
                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acid
                                                                                                                                                                                                      REGISTRATION NUMBER: 28,807
REFERENCE/DOCKET NUMBER: 06:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 322-5070
                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION: NAME: Bozicevic, Karl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Karl Bozicevic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Prusiner, Stanley B.
APPLICANT: Scott, Michael R.
APPLICANT: Telling, Glenn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                     FILING DATE: 3
CLASSIFICATION:
                                                                                                            TYPE: amino a STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Menlo Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56 GWGQPHGG 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
nes 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GWGQPHGG 8
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                                                                                                                            amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Application US/08692892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CA
                                                                                                                                         253 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2200 Sand Hill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      253 amino acids
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linear
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                                                 HUMAN PRION PROTEIN, HuPrP
                                                                                               linear
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                                                                           peptide
                                                                                                                                                                                                                                                                                                                      30-JULY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           peptide
                                                                                                            single
                                                                                                                                                                     3) 322
854-0875
NO: 2:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DETECTING PRIONS IN A SAMPLE AND PRION PREPARATION AND TRANSGENIC ANIMAL USED FOR SAME
   100.0%;
                                                                                                                                                                                                                                                                                                                                      us/08/692,892
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                                                                                                                                                                                                                                          06510/056001
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   Score 55;
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Pred. No. 0.22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                     Version
   DВ
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 1;
Length 253;
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-713-939A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/08713939A

Patent No. 5846533

GENERAL INFORMATION:

APPLICANT: Prusiner, Stanley B.
APPLICANT: Williamson, R. Anthony
APPLICANT: Burton, Dennis R.

TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP
NUMBER OF SEQUENCES: 86

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STREET: 2200 Sand Hill Road

CITY: Menlo Park

STATE: CA
Search completed: January 3, 2003, 15:34:26 Job time: 12 secs
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US-08-713-939A-2
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                                                                                                                                       Query Match
Best Local Similarity
Matches 8; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 100.0%; Pred. No. 0.22; Matches 8; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEO VETSION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/713,939A
FILING DATE: 13-SEP-1996
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                 NAME: Bozicevic, Karl
REGISTRATION NUMBER: 28,807
REFERENCE/DOCKET NUMBER: 0651
TELECOMPUNICATION INFORMATION:
TELEPHONE: 415-854-5277
TELEPAX: 415-854-0875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: U.S.A.
COUNTRY: U.S.A.
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                  1 GWGQPHGG 8
||||||||
56 GWGQPHGG 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GWGQPHGG 8
||||||||
56 GWGQPHGG 63
                                                                                                                                     nilarity 100.0%; Score 55; DB 2; Length 253; Conservative 0; Mismatches ?
                                                                      63
                                                                                                                                                                                                                                                                                                                                                                                                                                        06510/059001
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                                                                                                                                            0;
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                                                                                                                                          Gaps
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Database :
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Maximum DB seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       al number of hits satisfying chosen parameters:
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                             Published_Applications_AA: *

1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep: *

2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep: *

3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep: *

4: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep: *

5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep: *

6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep: *

7: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep: *

9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep: *

9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep: *

10: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep: *

11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep: *

12: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep: *

13: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep: *

14: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep: *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  length: 0
length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-543-188A-1
55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           January 3, 2003, 15:32:11; Search time 6.36364 Seconds (without alignments) 23.825 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      117078 seqs, 18951520 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GWGQPHGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GenCore version 5.1.3 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             117078
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SUMMARIES

Result	Score	, : Ch	Length	DB	ID	Description
N	55	100.0	43	10	US-09-147-761-2	Sequence 2
ω	55	100.0	253	10	US-09-904-987-3	Sequence
4	55	100.0	253	10	US-09-919-172-57	Sequence 57
υ	55	100.0	253	10	US-09-943-906-2	Sequence
σ	55	100.0	254	9	US-10-106-574-5	Sequence 5
7	55	100.0	254	9	US-10-106-574-6	Sequence 6,
œ	55	100.0	254	9	US-10-106-574-7	Sequence 7
9	55	100.0	254	9	US-10-106-574-8	Sequence 8,
10	55	100.0	254	10	US-09-943-906-1	Sequence :
11	55	100.0	255	10	US-09-943-906-4	Sequence,
12	55	100.0	256	9	US-10-109-551-2	Sequence 2
<u>1</u> 3	55	100.0	256	9	US-10-109-551-4	Sequence 4
14	55	100.0	256	9	US-10-109-551-6	Sequence 6
15	55	100.0	256	9	US-10-109-551-8	Sequence 8
16	55	100.0	256	9	US-10-109-551-10	Sequence 10
17	55	100.0	263	10	US-09-943-906-3	Sequence 3
18	55	100.0	439	9	US-10-115-984-2	Sequence 2,
19	46	83.6	20	3	115-10-035-598-1	Seguence

ALIGNMENTS

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RESULT 2
US-09-147-761-2
; Sequence 2, Application US/09147761
; Patent No. US20010010918A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
""tches 8; Conserve
                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Description of Artificial Sequence:prion protein ; OTHER INFORMATION: specific synthetic peptide US-09-939-780-2
                                                                                                                                                                                                           В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 1
US-09-939-780-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: O'CONDOY, Michael
APPLICANT: O'CONDOY, Michael
TITLE OF INVENTION: Immunological Assay for Spongiform Encephalopathies
FILE REFERENCE: 50002US
CURRENT APPLICATION NUMBER: US/09/939,780
CURRENT FILING DATE: 2001-08-28
CURRENT FILING DATE: 2001-08-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PATENTIN VEr. 2.1
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/09939780 Patent No. US20020168689A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 09/147,761
PRIOR FILING DATE: 1999-03-03
PRIOR APPLICATION NUMBER: PCT/IE98/00007
                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 43
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
APPLICANT:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                       15 GWGQPHGG 22
                                                                                                                                                                                                                                            1 GWGQPHGG 8
                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                       100.0%;
    IMMUNOLOGICAL ASSAY FOR SPONGIFORM ENCEPHALOPATHIES
                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                  Score 55; DB 9; Pred. No. 0.044; Mismatches 0
                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                          Length 43;
                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                      0;
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RESULT 4
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; CELL TYPE:
US-09-147-761-2
                                                           Вb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                В
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                                                                                                                                                                                     US-09-904-987-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 3
                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: No. US20020037908Alactyl, Inc.
TITLE OF INVENTION: Methods and Compositions for Controlling Pathological and Prepath
TITLE OF INVENTION: Protein Assembly or Aggregation
FILE REFERENCE: 42108/26146
CURRENT APPLICATION NUMBER: US/09/904,987
CURRENT FILING DATE: 2001-07-12
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.0
SEQ ID NO 3
LENGTH: 253
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/09904987 Patent No. US20020037908A1
                                                                                                                       Matches
                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                     ORGANISM: homo sapiens
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: NCBI ENTREZ / XM_009567
DATABASE ENTRY DATE: 2001-04-17
RELEVANT_RESIDUES: (1)..(253)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 353-1-6605033
TELEFAX: 353-1-6606920
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 4

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/147,761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 353-1-6605033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: HYPOTHETICAL:
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                                                                                         1 GWGQPHGG 8
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Pred. No. 0.044;
                                                                                                                                      Score 55; DB 10; Length 253; Pred. No. 0.21;
                                                                                                                       Mismatches
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Best Local S
Matches 8
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56 GWGQPHGG 63
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nes 8; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: CA
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APPLICANT: Fails, Mary
APPLICANT: Turner, Christopher M.
TITLE OF INVENTION: PROSTATE CANCER MARKERS
FILE REFERENCE: PA-0036 US
CURRENT APPLICATION NUMBER: US/09/919,172
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/222,469
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NO 57
SEQ ID NO 57
LENGTH: 253
TYPE: PRT
TYPE: PRT
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US-09-943-906-2
Sequence 2, Application US/09943906
Patent No. US20020150571A1
GENERAL INFORMATION:
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                   TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                           NAME: BOZICEVIC, KARI
REGISTRATION NUMBER: 28,807
REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-5277
TELEFAX: 415-854-0875
                                                                                                                                                                                                                                  APPLICATION NUMBER: 09/550,374
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARRE: PASTASEO Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/943,906
FILING DATE: 30-Aug-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 2200 Sand Hill Road
                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP NUMBER OF SEQUENCES: 86
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LENGTH: 253 amino acids
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Burton, Dennis R.
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TOPOLOGY: linear

HOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-943-906-2
RESULT 8
US-10-106-574-7
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US-10-106-574-6
                                                                                                                                                                                                    SEQ ID NO 6
LENGTH: 254
TYPE: PRT
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                                                                                                                                           Query Match
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Best Local S
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CURRENT FILING DATE: 2002-03-26
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                 RENERAL INFORMATION:
APPLICANT: Harris, David A.
APPLICANT: Stewart, Richard S.
TITLE OF INVENTION: Compositions and Methods for
FILE REFERENCE: 09789280.0003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENERAL INFORMATION:
APPLICANT: Harris, David A.
APPLICANT: Stewart, Richard S.
TITLE OF INVENTION: Compositions and Methods
FILE REFERENCE: 09789280.0003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/106,574
CURRENT FILING DATE: 2002-03-26
NUMBER OF SEQ ID NOS: 8
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les 8; Conserv
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Pred. No. 0.21;
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; TYPE: PRT
; ORGANISM: Murinae gen.
US-10-106-574-7
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US-09-943-906-1
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NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn version 3.1
SEQ ID NO 7
LENGTH: 254
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SEQ ID NO 8
LENGTH: 254
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Patent No. US20020150571A1
GENERAL INFORMATION:
APPLICANT: Prusiner, Stanley B.
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Matches 8; Conser
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Matches 8; Conserv
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CURRENT FILING DATE: 2002-03-26
NUMBER OF SEQ ID NOS: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Harris, David A.
APPLICANT: Stewart, Richard S.
TITLE OF INVENTION: Compositions and Methods
FILE REFERENCE: 09789280.0003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Stewart, Richard S. TITLE OF INVENTION: Compositions and Methods for the Study and Diagnosis of Prion FILE REFERENCE: 09789280.0003
CURRENT APPLICATION NUMBER: US/10/106,574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Harris, David A. APPLICANT: Stewart, Richar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 254
TYPE: PRT
ORGANISM: Murinae gen.
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                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 2200 Sand Hill Road
                                                                                                                                          TITLE OF INVENTION: ANTIBODIES SPECIFIC
COUNTRY: U.S.A.
ZIP: 94025
                                   CITY: Menlo Park
STATE: CA
                                                                                                                        OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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Burton, Dennis R.
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Pred. No. 0.21;
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COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible OPERATING SYSTEM: DOS

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RESULT 11
US-09-943-906-4
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Matches 8; Conser
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INFORMATION FOR SEQ ID NO: 1:
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FILING DATE: CUNKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: BOZLCEVIC, KATI
REGISTRATION NUMBER: 28,807
REGISTRATION NUMBER: 06510/0
TELEPHONE: 415-854-5277
TELEPHONE: 415-854-5277
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                                APPLICATION NUMBER: 09/550,374
FILING DATE: <UNKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: BOZICEVIC, Karl
REGISTRATION NUMBER: 28,807
REFERENCE/DOCKET NUMBER: 06510/059001
                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/943,906
FILING DATE: 30-Aug-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                        ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
TELECOMMUNICATION INFORMATION: TELEPHONE: 415-854-5277
                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 2200 Sand Hill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
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EILING DATE: 30-Aug-2001
CLASSLETICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: FastSEQ Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR NATIVE PrP NUMBER OF SEQUENCES: 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                              COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FastSEQ Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                    CITY: Menlo Park
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Prusiner, Stanley B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Williamson, R. Anthony Burton, Dennis R.
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Pred. No. 0.21;
; Mismatches 0;
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; ORGANISM: Ovis aries US-10-109-551-4
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US-10-109-551-2
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                                                                                                                                                                                                                                                                                      Sequence 4, Application US/10109551 Publication No. US20020194635A1 GENERAL INFORMATION:
                                                  SEQ ID NO 4
LENGTH: 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: DUNNE, P
APPLICANT: PIEDRAH
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Best Local Similarity
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                                                                                                                     APPLICANT: PIEDRAHITA, JORGE
TITLE OF INVENTION: TRANSGENIC ANIMALS RESISTANT TO TRANSMISSIBLE
TITLE OF INVENTION: SPONGIFORM ENCEPHALOPATHIES
FILE REFERENCE: TANK:207US
CURRENT APPLICATION NUMBER: US/10/109,551
CURRENT FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: 60/280,549
PRIOR FILING DATE: 2001-03-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: TRANSGENIC ANIMALS RESISTANT TITLE OF INVENTION: SPONGFORM ENCEPHALOPATHIES FILE REFERENCE: TAMK: 207US FORM ENCEPHALOPATHIES CURRENT APPLICATION NUMBER: US/10/109,551 CURRENT FILING DATE: 2002-03-28 PRIOR APPLICATION NUMBER: 60/280,549 PRIOR FILING DATE: 2001-03-30 NUMBER: 05 SEQ ID NOS: 10
                                                                                      SOFTWARE: PatentIn Ver. 2.1
                                                                                                          NUMBER OF SEQ ID NOS: 10
                                                                                                                                                                                                                                                     APPLICANT: DUNNE, PATRICK W. APPLICANT: PIEDRAHITA, JORG
                                   TYPE: PRT
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SEQUENCE CHARACTERISTICS:
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nes 8; Conserv
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MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
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Pred. No. 0.21;
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Pred. No. 0.21;
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APPLICANT: DUNNE, PATRICK W.

APPLICANT: PIEDRAHITA, JORGE
TITLE OF INVENTION: TRANSGENIC ANIMALS RESISTANT TO TRANSMISSIBLE
TITLE OF INVENTION: SPONGIFORM ENCEPHALOPATHIES
FILE REFERENCE: TAMK: 207US
CURRENT APPLICATION NUMBER: US/10/109,551
CURRENT FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: 60/280,549
PRIOR FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 8
LENGTH: 256
TYPE: PAT
ORGANISM: Odocoileus hemionus hemionus
Search completed: January Job time : 6.36364 secs
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US-10-109-551-8
: Sequence 8, Application US/10109551
: Publication No. US20020194635A1
: GENERAL INFORMATION:
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TYPE: PRT
ORGANISM: Odocoileus virginianus
US-10-109-551-6
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US-10-109-551-6
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Best Local S
Matches 8
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APPLICANT: PIEDRAHITA, JORGE
TITLE OF INVENTION: TRANSGENIC ANIMALS RESISTANT TO TRANSMISSIBLE
TITLE OF INVENTION: SPONGIFORM ENCEPHALOPATHIES
FILE REFERENCE: TAMK:207US
CURRENT APPLICATION NUMBER: US/10/109,551
CURRENT FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: 60/280,549
PRIOR APPLICATION NUMBER: 60/280,549
PRIOR FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 366
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59 GWGQPHGG 66
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59 GWGQPHGG 66
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Post-processing: Minimum Match 08
Maximum Match 10
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Maximum DB seq
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/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3, 2003, 15:21:45;
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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4 5	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17		15		13		11
<u>ω</u>	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	32	32	32	32	32	32	3 3	ω W	34	34
			•	•	•						•	•			•				•	•	91.2	•	•	•			94.1	94.1	94.1	94.1	97.1	97.1		100.0
118	116	100	91	80	69	65	47	45	42	21	21	21	21	20	20	20	20	20	20	20	20	20	16	12	484	251	177	142	128	128	301	298	754	55 4
21	22	21	22	21	22	21	23	21	22	23	23	22	18	22	22	22	22	21	20	19	19	12	17	19	22	22	22	16	20	15	20	20	23	22
AAY52541	AAU44203	AAY64671	AAU14672	AAY52548	AAU21012	AAB24836	AAM47704	AAB03863	AAB71931	AAU75379	AAU75372	AAB86331	AAW12384	AAE01995	AAE04428	AAE08740	AAE11049	AAY52559	AAY17756	AAW68295	AAW69959	AAR10540	AAR84070	AAW60537	ABG05597	AAU33248	AAU15989	AAR81311	AAY28360	AAR53332	AAY24022	102	80 1	AAU14133
KappaLAMP-Th fusio	Propionibacterium	Human 5' EST relat	Novel bone marrow	Murine Ig-kappa si	Human novel foetal	ŭ	Fragment of a reco	Active human neuro	Murine sig-mEndo f	immun	Mouse kappa immuno	Ig-kappa chain lea	Murine Ig kappa-ch	Immunoglobulin (Ig	Human immunoglobul	obulin ka	Human Ig (immunogl	us muri	rget signal p		Ig kappa chain lea	Eukaryotic signal	Plasmid pBlue-TH6		human	human	Human novel secret	Rat monoclonal ant		a.	35-H9	5	cidally acti	Human novel protei

ALIGNMENTS

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RESULT 1
AAU11826
                                                                                                                                                                                                                                     Prion protein; Prp; ligand; octapeptide motif; scrapie; prion-associated disease; Creutzfeldt-Jakob disease; Gerstmann-Straussler-Scheinker disease; fatal familial insomnia;
          WPI; 2002-061944/08
                                  Hammond DJ, Wiltshire VR,
                                                                                05-APR-2000; 2000US-0543188
                                                                                                                                                        WO200177687-A2.
                                                                                                                                                                                                      chronic wasting
                                                                                                                                                                                                                                                                                                                                         AAU11826;
                                                                                                                                                                                                                                                                                                                                                                AAU11826 standard; peptide; 6 AA.
                                                                                                        05-APR-2001; 2001WO-US11150
                                                                                                                                18-OCT-2001.
                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                feline spongiform encephalopathy; bovine spongiform encephalopathy;
transmissible mink encephalopathy; exotic ungulate encephalopathy;
                                                                                                                                                                                                                                                                                        Peptide ligand for Prion protein, PrP, #1.
                                                                                                                                                                                                                                                                                                                 26-MAR-2002 (first entry)
                                                        ۷Ι
                                                        TECHNOLOGIES INC
                                                                                                                                                                                                       disease
                                  Carbonell R,
                                  Shen H;
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RESULT 2
ABB40848
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a ligand of less than 6 kD that binds to a polypeptide containing the sequence GlyTyrGlyGlnProHisGlyGly (A) or an analogue that is the retro-inverso isomer of (A). The sequence A is an octapeptide motif from the prion protein (PrP). The ligands are identified by binding assays with the peptide (A) or peptides containing (A). The ligands are used for detecting prion proteins (or prions) in biological or environmental samples, e.g. for diagnosis, also for removing them from samples, for treating or retarding development of prion-associated diseases, especially Creutzfeldt-Jakob diseases (in latrogenic, new variant, familial resonable, familial insomnia, scrapie, bovine or feline spongiform encephalopathy, transmissible mink or exotic ungulate encephalopathy, or chronic wasting disease. The
measuring human gene expression in a sample derived
                     The invention relates to a single exon nucleic acid
                                                  Claim
                                                                         anaryzing
                                                                                                                 WPI; 2001-483447/52.
                                                                                                                                                                     (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                           Human; foetal
                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABB40848;
                                                                                                                                           Penn
                                                                                                                                                                                                04-OCT-2000;
                                                                                                                                                                                                                                     03-AUG-2000;
                                                                                                                                                                                                                                                26-MAY-2000;
                                                                                                                                                                                                                                                                           04-FEB-2000;
                                                                                                                                                                                                                                                                                                     30-JAN-2001; 2001WO-US00669
                                                                                                                                                                                                                                                                                                                               09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                        WO200157277-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide #8354 encoded by human foetal liver single exon probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABB40848 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                present sequence is a ligand of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 16; Page 34;
                                                                                                                                                                                                           21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New ligands for prion proteins, useful for detection or removal or prions and for treating prion-associated diseases, recognize a specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ľ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 LLIWIP 6
                                                                                                                                                                                                                                                                                                                                                                                 sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LLIWIP 6
                                                                         genome-derived single exon nucleic zing gene expression in human fetal
                                                                                                                                                                     MOLECULAR DYNAMICS INC
                                                 SEQ
                                                                                                                                          Hanzel
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                                                                                                                                                                                                        2000US-0180312.
2000US-0207456.
2000US-0508408.
2000US-0533667.
2000US-0234687.
2000US-0236359.
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                                                                                                                                                                                               2000GB-0024263
                                                 IJ
                                                                                                                                                                                                                                                                                                                                                                                                        liver; gene expression; single exon nucleic acid probe
                                                                                                                                          DK,
                                                 NO 33483;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
                                                                                                                                           Chen
                                              639pp + sequence listing;
                                                                                                                                          ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 34; DB zs;
Pred. No. 7.8e+05;
                                                                                                                                          Rank
                                                                                                                                          DR
                                                                         acid probes
liver -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
         probe for
from human foetal
                                              English.
                                                                                      useful
                                                                                        for
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ABB25012
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                      04 - FEB - 2000;
26 - MAY - 2000;
30 - JUN - 2000;
03 - AUG - 2000;
                      By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and congenital heart disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                      measuring human gene expression in a sample derived from human heart (see ABA21535-ABA41305). The present sequence is a protein encoded by one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                               The present invention relates to single exon
                                                                                                                                                                                            Claim 15;
                                                                                                                                                                                                                                   Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 congenital heart disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB25012;
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                                                                                                                                                                                                                                                                                                                                                             21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-JAN-2001; 2001WO-US00666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200157274-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cardiovascular disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; gene expression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein #7011 encoded by probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABB25012 standard;
                                                                                                                                                                                                                                                                                                                    (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48
           ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 LLIWIP 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LLIWIP
                                                                                                                                                                                                                                                                                         SG
                                                                                                                                                                                                                                   exon nucleic acid probes for analyzing gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 6; Conser
                                                                                                                                                                                                                                                                                                                    MOLECULAR DYNAMICS INC
                                                                                                                                                                                            SEQ
                                                                                                                                                                                                                                                                                         Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87
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                                                                                                                                                                                                                                                                                                                                                        2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                               2000GB-0024263
                                                                                                                                                                                            ID No 26782;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein;
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                                                                                                                                                                                                                                                                                         Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypertension; cardiac arrhythmia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             heart; microarray; vascular system;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .0%;
                                                                                                                                                                                         530pp;
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Pred.
                                                                                                                                                                                                                                                                                         Rank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for measuring heart cell gene expression.
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                                                                                                                                                                                           English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34;
No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22;
                                                                                                                                                                 nucleic acid probes for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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RESULT 5
AAM74503
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Best Local Similarity
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                                                               Matches
                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                               03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                    probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of
                                                                                                                                                                                                                                       Penn
                                                                                                                                                                                                                                                                                                                                                                                                            Human; brain expressed exon; gene expression analysis; probe;
microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                               Sequence
                                                                                                                                                                                                       Single
                                                                                                                                                                                                                                                                                                     04-FEB-2000; 2000US-0180312.
26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Human brain expressed single exon probe encoded protein SEQ ID NO: 33812
                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAM61707 standard;
                                                                                                                                                                              Example 4; SEQ ID NO:
                                                                                                                                                                                                                                                     (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                      09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                      WO200157275-A2
                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                      epilepsy; cancer.
                                                                                                                                                             The present invention provides a number of single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                     30-JAN-2001; 2001WO-US00667
                                                                                                               the probes of the invention.
                                48 LLIWIP 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48 LLIWIP 53
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                                              1 LLIWIP 6
                                                                                                                                                                                                                                      SG,
                                                                                                                                                                                                     exon nucleic acid
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                                                                                                                                                                                                                                                                    2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0234639.
2000US-0236359.
                                                                Conservative
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                                                                                               AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     entry)
                                                                      100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
                                                                                                                                                                             33812; 650pp + Sequence Listing;
                                                                                                                                                                                                                                      Chen W,
                                                                                                                                                                                                     probes
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                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87
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Pred. No.
                                                                      Score 34;
Pred. No.
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                                                                                                                                                                                                    for analyzing gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                               Mismatches
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                                                                               22;
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                                                                               Length 87;
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                                                               Indels
                                                                                                                                                                             English
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                                                                                                                     RESULT 6
AAM34616
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                                                                                                                                                                                             Query Match
Best Local :
                                       genetic
                                                                                                                                                                                                                     Sequence
      WO200157272-A2
                                                                                               AAM34616;
                                                                                                                                                                                                                                                                                             Example 4;
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04 FEB-2000; 2000US-0180312.
26 MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234587.
27-SEP-2000; 2000US-0236559.
04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probes which are derived from
bone marrow. They can be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-488900/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           microarray; cancer;
Homo sapiens
                                                            Probe; microarray;
                                                                                                 Peptide #8653 encoded by probe for measuring placental gene
                                                                                                                                              17-OCT-2001
                                                                                                                                                                                                                              AAM34616 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention provides a number of single exon nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                analyzing gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; bone marrow expressed exon; gene expression analysis; probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human bone marrow expressed probe encoded protein SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAM74503 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200157276-A2
                                                                                                                                                                                                                                                                                                                               1 LLIWIP 6
||||||
48 LLIWIP 53
                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity tes 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  genome-derived single exon nucleic acid probes useful for zing gene expression in human bone marrow -
                                           disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO: 34809; 658pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2001WO-US00668
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                                                              human; placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             leukaemia; lymphoma; myeloma.
                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chen W,
                                                                                                                                                                                                                              87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rank
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          34;
                                                              antenatal diagnosis;
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                                                                                                   expression.
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Best Local S
Matches 6
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-FEB-2000; 2000US-180312P-
26-MAY-2000; 2000US-207456P-
30-JUN-2000; 2000US-0608408-
03-AUG-2000; 2000US-0632366-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         see AAI31315-AAI57546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                             chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; Gaucher's disease; pulmonary histocytosis; lymphangioleiomyomtosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia; pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
                                                                                                                                                                                                                                                              WO200186003-A2
                                                                                                                                                        30-JAN-2001; 2001WO-US00665
                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; single exon probe; asthma; lung cancer; COPD; ILD, chronic obstructive pulmonary disease; interstitial lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABG44369 standard; Peptide; 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2001-488897/53.
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                                                                                                                                                                                                                                                                                                                                                                  membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                       ciliary dyskinesis; pulmonary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene expression in human placenta
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2000US-0207456.
2000US-0608408.
2000US-0632368.
2000US-0234687.
2000US-0234687.
2000US-02346359.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           encoded by genome-derived single exon probe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               No 34885; 654pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 34;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rank DR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                     Complements of the 12307 Open reading traines derived from the 1201 of probes; the novel set of probes which hybridise at high stringency to a collectic acid expressed in the human lung; measuring gene expression in a casample derived from human lung; comprising (a) contacting the array with Ca a collection of detectably labeled nucleic acids derived from human lung comprising (a) algorithmically predicting at least one exon from genomic sequences (a) algorithmically predicting at least one exon from genomic sequences (c) the array; identifying exons in a eukaryotic genome, comprising (a) identifying exons in a eukaryotic genome, comprising (c) in the above mentioned microarray; assigning exons to a single exon probe, thaving a fragment identifying exons from genomic sequence by the method comprising (a) identifying exons from genomic sequence by the method above and (b) measuring the expression of each of the exons in several comprising (a) identifying exons from genomic sequence by the method cabove and (b) measuring the expression of each of the exons in several comprising one confirm the exons in sequence by the method cabove and (b) measuring the expression of each of the exons in several confirmation of the exons in several confirmation of each of the exo
                                                                                                                             Query Match
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from human lung comprising single exon nucleic acid probes hav
12614 nucleic acid sequences mentioned in the specification, c
complements or the 12387 open reading frames derived from the
                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim
                                                                                                                                                                                                                                                                                                                                    ftp.wipo.int/pub/published_pct_sequences.
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48
                                                           1 LLIWIP 6
LLIWIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27; SEQ ID No 34034; 634pp; English.
                                                                                                                             6; Conserv
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53
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2000US-236359P.
2000GB-0024263.
                                                                                                                                Conservative
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Pred. No.
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CHAPTER DETERMINATION OF DETERMINATION OF
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                  WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              odorant receptor DOR59. The odorant genes and proteins, such as those provided by the invention, are useful as they aid in the study of the olfactory organ in mammals, as well as adding the understanding of the link between odour recognition and behaviour in insects. They also enable the identification of compounds capable of activating and inhibiting the receptors, allow the control of pest populations via the use of alarm odour ligands and via the use of ligands which interfere with the interaction between odorant ligands and receptors associated with
     23-MAR-2000; 2000US-191637P
11-JUL-2000; 2000US-0614150
                                                                                                                                              27-SEP-2001
                                                                                                                                                                                                                                                  Drosophila melanogaster
                                                                                                                                                                                                                                                                                                           pharmaceutical.
                                                                                                                                                                                                                                                                                                                                        Drosophila;
                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster polypeptide SEQ'ID NO 32961.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-572081/53.
N-PSDB; AAA94845.
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                                                                                     23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB68723 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is the previously identified Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vosshall LB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UYCO ) UNIV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24 LLIWIP 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 LLIWIP 6
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                                                                                                                                                                                                                                                                                                                                     developmental biology;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                     cell
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1.7e+02;
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AAB20922
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Odorant receptor; Drosophila; olfactory receptor; grotein-coupled receptor; GPCR superfamily; transgenic insect; insect behaviour modification; pest control; pollinator attraction; biosensor; odour detection; odour identification; apiculture.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated nucleic a genes from Drosophila interactions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invent
                                           New nucleic acid encoding a Drosophila olfactory receptor, useful identifying modulating agents -
                                                                                                                                                                                                         Carlson JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200043410-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila odorant receptor DOR 56E.1.
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                                                                                                                             N-PSDB;
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                                                                                                                             2000-543246/49.
DB; AAA72257.
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                                                                                                                                                                                                      Kim J,
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Pred. No. 1.7e+02;
; Mismatches 0;
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Claim 12; Page 175-177; 303pp; English

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S S S X S X B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CC which modulate expression of these genes, and in methods to identify creeptor binding partners. The Drosophila odorant receptor nucleic acids CC may also be used to identify corresponding genes in other insects, cs such as those which damage crops or transmit disease. The odorant CC receptor proteins may be used to identify agents which modulate their CC activity, to identify binding partners, as antigens to raise antibodies, CC and in methods to modify insect behaviour. The proteins may be also be used in methods of behaviour modification. Such methods may be used CC to study or modify insect behaviour in response to odorants such as CC pheromones. Modification of insect behaviour has a wide range of applications, such as in pest control (e.g., by disrupting the feeding or mating behaviours of pest species), or for enhancing plant CC and/or nucleotides may also be used to identify appetite suppressants, to trap odours of a specific type, as biosensors for the detection of CC explosives, drugs, perfumes or pollutants, and in apiculture to modify the behaviour of bees, for example, to increase the production of royal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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Best Local
N-PSDB; AAS22438.
                                                            Tang
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                                                                                                                                                                                                                                                                                                                                                                                           immunomodulatory; cytostatic; neuroprotective; vulnerary; nootropic; anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiviral;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human novel protein
                                                                                                                                     25-JAN-2000; 2000US-0491404
                                                                                                                                                                       25-JAN-2001; 2001WO-US02623
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                                                                                                                                                                                                                                                 WO200155437-A2
                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                       thrombolytic; immunoc
Parkinson's disease;
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                                                                                                 (HYSE-)
                                                                                                                                                                                                                                                                                                                                                                           antibacterial; antiallergic;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; novel protein; Antianaemic; osteopathic; antiinflammatory;
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                          2001-451939/48.
                                                                                                                                                                                                                                                                                                                        regeneration;
                                                                                                 HYSEQ
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immunogen; antibody; gene therapy; neurological disorder;
ilsease; inflammatory disorder; cancer; asthma; osteoporosi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 453;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                         asthma; osteoporosis;
                                                                                                                                                                                                                                                                                                                                                                             antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
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δÃ
В
                                                                                                                                                                                                                                             The invention relates to polynucleotides encoding novel human CC proteins or their active domains. The polypeptides, polynucleotides and CC antibodies raised against the polypeptides are used in a method of CC treatment of a mammal and prevention of disorders caused by the aberrant CC protein expression or activity. The polypeptides can be used as CC molecular weight markers, food supplements, and in antibody production. CC The polypeptides are used to identify compounds which bind to the CC polypeptides. Polynucleotides of the invention are used as probes and CC primers, for sequencing, for chromosome or gene mapping, in the CC production of recombinant proteins, and in generating anti-sense DNA or CC RNA and in gene therapy. Polypeptides of the invention can be used to carget drugs to a tumour, in assays to determine biological activity, to CC target drugs to a tumour, in assays to determine guantitative CC crise antibodies/elicit an immune response, to determine quantitative CC polypeptides of the invention may also be useful in treating platelet CC polypeptides, as tissue markers, and to isolate receptors or ligands. CC disorders, stem cell disorders, regenerating bone, cartilage, tendon, CC ligament and/or nerve tissue, wound healing, treating burns, promoting CC the proliferation, differentiation and survival of stem cells, as a contraceptive, treating osteoporosis and osteoarthritis, anaemia, CC Alzheimer's, Parkinson's and Huntington's diseases, amylotrophic lateral crisciples is a contracted to the contracte
                                                                                                                      Matches
                                                                                                                                                   Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                              fungal infection or from autoimmunity, cancer, allergy, asthma, graft-versus-host disease, eczema, haemophilia, thrombosis, anti-inflammatory diseases, nervous system disorders, and infec
                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                    The present sequence represents a protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                              sclerosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nervous system disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolated polypeptides useful for treating anti-inflammatory diseases,
138 LLIWIP 143
                                                         1 LLIWIP 6
                                                                                                                      Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                           stroke, immune deficiencies resulting
                                                                                                                                                                                                                                          554 AA;
                                                                                                                      Conservative
                                                                                                                                             100.0%; Score 34; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          894pp; English.
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                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for regenerating bone and cartilage
                                                                                                                      Mismatches
                                                                                                                                                                                   DB 22;
                                                                                                                                                   .5e+02;
                                                                                                                                                                             Length 554;
                                                                                                                                                                                                                                                                                                                                                                                                                        from bacterial, viral
                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                    infection
                                                                                                                   0;
                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                              or
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ABB92828
                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 12
                              Tietjen
                                                                                                                                                                                                                                                              Herbicidal;
                                                                                                                                                                                                                                                                                                                              31-MAY-2002
                                                                                                                                                                                                                                                                                                                                                             ABB92828;
                                                                                                                                                                                                                                                                                                                                                                                             ABB92828 standard; Protein; 754 AA
WPI; 2002-269010/31.
                                                              (FARB ) BAYER AG
                                                                                              28-AUG-2001; 2001WO-EP09892
                                                                                                                               28-AUG-2001; 2001WO-EP09892
                                                                                                                                                                                             WO200210210-A2
                                                                                                                                                                                                                              Arabidopsis thaliana
                                                                                                                                                                                                                                                                                           Herbicidally active polypeptide SEQ ID NO 2039.
                              ζ,
                              Weidler
                                                                                                                                                                                                                                                            plant;
                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                            agriculture;
                                                                                                                                                                                                                                                              herbicide
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DT PT XXX

Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences

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RESULT 13
AAY24023
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    atches
            The present sequence represents a novel receptor, CMRF-35-H9, which binds immunoglobulin M (IgM). CMRF-35-H9, a CMRF-35-H9 extracellular domain peptide or a vector encoding these, can be used to modulate an immune response in a patient or to block or inhibit a humoral immune response in a patient of the sequence of the sequence of the patient who has or is about to receive a transplant. The CMRF-35-H9 receptor or extracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       suitable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding the are useful for identifying modulators. The identified modulators are
                                                                                                         Claim
                                                                                                                                                                                                                                                                                          14-JAN-1999;
                                                                                                                                                                                                                                                                                                                                             WO9936438-A1
                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using
                                                                                                                                             Human immunoglobulin M
                                                                                                                                                                     N-PSDB; AAX86359
                                                                                                                                                                                                                                                                14-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                          HOMO
                                                                                                                                                                                                                                                                                                                                                                                                                                                 promyelocytic leukemia; leukemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CMRF-35-H9 receptor; immunoglobulin M; IgM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY24023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY24023 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from plant with nucleic acid or
                                                                                                                                                                                                                                      (ORDE-) ORDER
                                                                                                                                                                                                                                                                                                                   22-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human CMRF-35-H9 receptor protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim
                                                                                                                                  immunomodulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                              humoral immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ||||||
19 LLIWIP 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity es 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 LLIWIP 6
                                                                                                                                                                                    1999-458446/38
                                                                                                        ω,
                                                                                                        Page 33; 40pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                herbicides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
    to antibodies,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                       Q.
                                                                                                                                                                                                                                                                98NZ-0329582
                                                                                                                                                                                                                                                                                          99WO-NZ00003
                                                                                                                                                                                                                                                                                                                                                                                                                                                              response; transplant; myeloid leukemia
                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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                                                                                                                                                                                                                                      SISTERS OF MERCY
                                                                                                                                                                                                                                                                                                                                                                     /note= "encoded by CTC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein; 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2039;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100
                                                                                                                                             receptor CMRF-35-H9, useful for
                                                                                                        English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           261pp +
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 34;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid sequences from non-plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
e CMRF-35-H9 receptor are then no longer fr
                                                                                                                                                                                                                                      IN QUEENSLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4.7e+02;
thes 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immunomodulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 754;
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 free to
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 bind
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transplant. A ligand/antigen construct that binds CMRF-35-H9 can to load a protective antigen or a stimulatory antigen into an ant presenting cell. The level of CMRF-35-H9 in a patient sample can determined to diagnose myeloid leukemia in a patient. An increase of CMRF-35-H9 or decreased level of promyelocytic leukemia is dia of leukemia.
The present sequence represents a novel receptor, CMRR-35-H9, which binds immunoglobulin M (IgM). CMRR-35-H9 a CMRR-35-H9 extracellular domain peptide or a vector encoding these, can be used to modulate an immune response in a patient or to block or inhibit a humoral immune response in a patient. This is particularly useful in a patient who has or is about to receive a transplant. The CMRR-35-H9 receptor or extracellular domain binds to antibodies, which are then no longer free to bind to the
                                                                                            Claim
                                                                                                                                                    N-PSDB; AAX86358
                                                                                                                                                               WPI; 1999-458446/38
                                                                                                                                                                                       Hart DNJ
                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           promyelocytic leukemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      humoral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human CMRF-35-H9 receptor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY24022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                         14-JAN-1999;
                                                                                                                                                                                                                                                                                                                                        Region
                                                                                                                                                                                                                                                                                                                                                                                      Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CMRF-35-H9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY24022 standard; Protein;
                                                                                                                  immunomodulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       æ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LLIWVP 13
                                                                                           12;
                                                                                                                              immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
5; Conserv
                                                                                          Fig 2; 40pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                             OF SISTERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       response;
                                                                                                                                                                                                                                                         99WO-NZ00003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA;
                                                                                                                                                                                                                                    98NZ-0329582
                                                                                                                                                                                                                                                                                                                                                                                                               10
                                                                                                                                                                                                                                                                                                                                        /note= "putative IgM binding domain" 178...201
                                                                                                                                                                                                                                                                                                                                                                        14..301
/label= mature_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                            /note=
                                                                                                                                                                                                                                                                                                                                                                                                 'note=
                                                                                                                                                                                                                                                                                                                                                                                                                      /label= signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97.1%;
83.3%;
                                                                                                                            M receptor CMRF-35-H9,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immunoglobulin M; IgM; immunomodulation;
                                                                                           English
                                                                                                                                                                                                                                                                                                                             "transmembrane region"
                                                                                                                                                                                                                                                                                                                                                                                               "encoded by CTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              leukemia
                                                                                                                                                                                                             OF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transplant;
                                                                                                                                                                                                             MERCY IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 33; DB Pred. No. 2.8e

1; Mismatches
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                                                                                                                                                                                                            QUEENSLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      myeloid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 20;
2.8e+02;
                                                                                                                              useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Leukemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 298,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              increased level
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RESULT 15
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Best Local Similarity
Thes 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transplant. A ligand/antigen construct that binds CMRF-35-H9 can be used to load a protective antigen or a stimulatory antigen into an antigen presenting cell. The level of CMRF-35-H9 in a patient sample can be determined to diagnose myeloid leukemia in a patient. An increased level of CMRF-35-H9 or decreased level of promyelocytic leukemia is diagnostic of leukemia.
                 isolated from hybridomas producing a mouse or rat monocional Ab reacting with the ganglioside GM2 respectively into an expression vector for use in animal cells which contains the human Ab heavy is
                                                             Chimeric human Ab expression vectors are constructed by inserting the Ab heavy and light chain variable region-encoding cDNA
                                                                                                             Disclosure;
                                                                                                                                        Humanised antibody specific for ganglioside GM2 - used for producing a cytocidal effect on cancers such as melanoma, neuroblastoma and glioma.
                                                                                                                                                                                                       WPI; 1994-126857/16.
N-PSDB; AAQ45430.
                                                                                                                                                                                                                                                     Shitara K;
                                                                                                                                                                                                                                                                                                                                                          07-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                        17-MAR-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                      AU9346181-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Monoclonal antibody; Ab; ganglioside GM2; chimera; chimeric antibody; expression vector; heavy; light; chain; hypervariable region; CDR; constant region; hybridoma; Ig; immunoglobulin; KM-796; KM-750; KM-603; cancer.
                                                                                                                                                                                                                                                                                                                             07-SEP-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR53332;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR53332 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                   Hanai N,
                                                                                                                                                                                                                                                                                            (KYOW ) KYOWA HAKKO KOGYO KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rat rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KM-603 light chain.
light chain constant region-encoding cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 LLIWVP 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 LLIWIP 6
                                                                                                                                                                                                                                                                 Hasegawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301
                                                                                                             Page 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label- sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label - CDR1
70..76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= CDR2
109..117
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83.3%;
                                                                                                           191pp;
                                                                                                                                                                                                                                                                   Koike
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 33; DB 20; L
Pred. No. 2.8e+02;
"''^matches 0;
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                                                                                                           English.
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Search completed: January
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Matches 5
                                                                                                                                                                                                                                                                                            are introduced into animal cells and the transformant thus obtained is cultured for the prodn. of a chimmeric human Ab reacting with the ganglioside GM2. In contrast to mouse monoclonal Abs, the chimmeric human Abs will not cause anti-mouse Ig Ab prodn. in the patient's body but show a prolonged blood half-life, with a reduced frequency of adverse effects, so that it can be expected to be superior to mouse monoclonal Abs in the efficacy in the treatment of human cancer, for instance.
                                                                                                                                                                                                                                             Mouse anti-GM2 monoclonal Ab KM-796 and KM-750 and rat KM-603 heavy and light chain sequences are given in AAQ45426-30. CDR regions for use in chimeric Abs are indicated in the
                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                 Features Table.
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GenCore version (c) 1993 - 2003
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[4847]

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A; Status: preliminary; nucleic acid sequence not shown; translation not shown

RESULT S65973

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1 LLIWIP 6 LLIWIP

A; Gene: yveQ

Best Local Similarity Matches 6; Conser

100.0%; ilarity 100.0%; Conservative

0;

Score 34; DB Pred. No. 64; 0; Mismatches

64; DB 2; 0;

Length 367;

0;

Gaps

0;

Query Match

Genetics:

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A;Cross references: EMBL:D26185; NID:g467326; PIDN:BAA05179.1; PID:g467333
A;Cross references: EMBL:D26185; NID:g467326; PIDN:BAA05179.1; PID:g467333
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1993
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1993
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1993
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1993
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1993
A;Note: the nucleotide sequence of the Gram-positive bacterium Bacillus subtilis.
A;Note: the nucleotide sequence of the Gram-positive bacterium Bacillus subtilis.
A;Cross references.
A;
                                                                                                                                                                                   C;Keywords: grycos/......
E;60-77/Domain: transmembrane #status
                                                                                                                                                                                                                                             A;Description: involved in surface protein binding to the membrane via glycosyl-phosphat A;Pathway: GPI-anchor biosynthesis C;Keywords: glycosyltransferase; hexosyltransferase; transmembrane protein
                                                                                                                                                                                                                                                                                                                                              A; Cross-references: GDB: 9956843; A; Map position: 15q21-15q22 C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Homo sapiens (man)
C;Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 03-Jun-2002
                                S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:D42138; NID:g1552168; PIDN:BAA07709.1; PID:g1552169
A;Experimental source: cell line P39
A;Note: part of the genomic DNA was also sequenced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Accession: S71751

9.TRKAhashi, M.; Inoue, N.; Ohishi, K.; Maeda, Y.; Nakamura, N.; Endo, Y.; Fujita, T.; To J. 15, 4254-4261, 1996

O J. 15, 4254-4261, 1996

A;Reference number: S71751; MUID: 97015126; PMID: 8861954

A;Accession: S71751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   dolichyl-phosphate-mannose-glycolipid alpha-mannosyltransferase (EC 2.4.1.130) PIGB - h. N.Alternate names: membrane protein PIG-B; phosphatidyl-inositol glycolipid biosynthesis
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                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Gene: GDB: PIGB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Genetics
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A; Residues: 1-554 <TAK>
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A; Start codon: TTG
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A; Residues: 1-402 <OGA>
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                                1 LLIWIP 6
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                                                                                             Similarity 6; Conserv
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ilarity 100.0%;
Conservative (
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Conservative
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69;
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                                                                                                                                                                                hypothetical protein C0805w - malaria parasite (Plasmodium falciparum)
C;Species: Plasmodium falciparum
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Superfamily: Plasmodium DNA-directed RNA polymerase II large chain C;Keywords: DNA binding; nucleotidyltransferase; phosphoprotein; tanc F;68-84/Region: zinc finger CCHH motif F;68-84/Region: 7-residue repeats
                            A; Reference number: 218935
A; Accession: T18492
                                                                                      R; Lawson, D.; Bowman, S.; Barrell, submitted to the EMBL Data Library,
                                                                                                                                                          C; Accession: T18492
                                                                                                                                                                                                                                                                                    T18492
                                                                                                                                                                                                                                                                                                                 RESULT 6
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A; Residues: 1-2452 <LIW>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Li, W.B.; Bzik, D.J.; Gu, H.; Tanaka, M.; Fox, B.A.; Inselburg, Nuccleic Acids Res. 17, 9621-9636, 1989.
A;Title: An enlarged largest subunit of Plasmodium falciparum RNA A;Reference number: S07485; MUID:90098832; PMID:2690004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Accession:
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C;Accession: S07485
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A;Molecule type: DNA
A;Residues: 1-754 <STO>
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Nature 402, 769-777,
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA-directed RNA polymerase (EC 2.7.7.6) II large chain - malaria parasite (Plasmodiu
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preliminary; translated
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   from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 34; DB 1;
Pred. No. 3.9e+02;
Mismatches 0;
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Pred. No. 1.3e+02;
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C;Superfamily: rabbit adult-specific brush border protein
C;Keywords: intestine; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-304 <FUL>
A; Cross-references: EMBL:U40829; NID:g1066476;
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A; Residues: 1-171 <BOL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Boll, W.; Schmid-Chanda, T.; Semenza, G.; Mantei, J. Biol. Chem. 268, 12901-12911, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Вb
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A; Note: C0805w
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A; Residues: 1-2457 <LAW>
                                                                                                                                                                                                                                   F;160-176/Domain:
                                                                                                                                                                                                                                                                                       A; Map position: 16R
                                                                                                                                                                                                                                                                                                                         A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                     A; Gene: MIPS: YPR147c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Reference number: S69022
A;Accession: S69034
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Genetics
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                                                                                                                                                                                                                                                                                                                                                                                       C;Genetics
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Matches
                                                                                                                 Matches
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Best Local S
                                                                                                                                                                                                                                                               Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pecies: Saccharomyces cerevisiae
Jate: 22-Aug-1996 #sequence_revision 06-Sep-1996 #text_change 19-Apr-2002
Accession: S69034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pecies: Oryctolagus cuniculus (domestic rabbit)
Date: 03-May-1994 #sequence_revision 03-May-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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31
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LLVWIP 36
                                                       LLIWIP 6
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83.3%;
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                                                                                                              Score 33; DB
Pred. No. 81;
1; Mismatches
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Pred. No. 3.9e+02;
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cosmid 9659
                                                                                                                                                                                                                                                                                                                                                                                                            PID:g1066494; GSPDB:GN00016; MIPS:YPR147c
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                                                                                                                                                                                                                                      <MMT>
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                                                                                                                                                                      Length 304;
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Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bar, Reference number: A83650; MUID:20512582; PMID:11058132 A;Accession: G83834
                                                                                                                                                                                                                                                                                             RESULT 11
T15500
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Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their
A;Reference number: $40312; MUID:94080891; PMID:8258341
A;Accession: $40312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Homo sapiens (man)
C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S40312
                       A; Molecule type: DNA
A; Residues: 1-269 <N
                                                               A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                      submitted to the EMBL Data Library, March 1995
A;Description: The sequence of C. elegans cosmid C15B12
A;Reference number: Z18362
A;Accession: T15500
                                                                                                                                                                               R; Nhan,
                                                                                                                                                                                                  C; Accession:
                                                                                                                                                                                                    hypothetical protein C15B12.2 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #tey C;Accession: T15500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:AP001512; GB:BA000004; NID:g10174030; PIDN:BAB05198.1; GSPDB:GA;Experimental source: strain C-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-200 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Accession: G83834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein BH1479 [imported] - Bacillus halodurans (strain C-125) C; Species: Bacillus halodurans C; Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;29-108/Domain: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:X72422; NID:g441312; PID:g441313 C;Superfamily: immunoglobulin V region; immunoglobulin hor C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1.126 < KLE>
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A;Cross-references: EMBL:U23529; NID:g746592; PID:g746594; PIDN:AAC46577.1; CESP:C15B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Status: preliminary
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Best Local (
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                   193 LLIWLP 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BH1479
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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83.3%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                         20-Sep-1999 #text_change 04-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32;
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immunoglobulin homology
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53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB
83;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 126,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bacterium Bacillus halodurans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypermutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S. submitted to GenBank, June 2000

A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigu chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, F.G.; Nunes, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak, A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silvai, M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z. M.; Silvai, M.R.; Vettore, A.L.; Z. M.; Silv
                                                                                                                                                                                                                                            hypothetical protein C40C9.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct.1999 #sequence_revision 15-Oct.1999 #text_change 18-Feb-2000
C;Accession: T19862
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A; Residues: 1
          A; Molecule type: DNA
A; Residues: 1-542 <WIL>
                                                                        A;Reference number: Z19188
A;Accession: T19862
A;Status: preliminary; translated
                                                                                                                                                                               R;Hembry, C. submitted to the EMBL Data
                                                                                                                                                                                                                                                                                                                                                                                  T19862
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Š
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C; Superfamily: Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Experimental source: C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 13
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Best Local Similarity
"" hes 5; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Contents: annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Experimental source: strain 9a5c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references: GB: AE003884;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Residues: 1-501 <SIM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: G82822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 406, 151-157, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Species:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         H2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 (similarity) - Xylella
pecles: Xylella·fastidiosa
ate: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 03-Jun-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               uperfamily: NADH dehydrogenase (ubiquinone) chain
sywords: membrane-associated complex; NAD; oxidore
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    XF0317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LLIWLP 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
5; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94.1%;
83.3%;
                                                                                                                                                                           Library,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 32;
Pred. No.
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Pred. No.
                                                                              from GB/EMBL/DDBJ
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l; Mismatches
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ns hypothetical protein C15B12.2
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1.1e+02;
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                                                43-108/Disulfide
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Biol. Chem. Hoppe-Seyler 369, 601-607, 1988

A;Title: Two unusual human immunoglobulin V-kappa genes
A;Reference number: S00996; MUID:89134397; PMID:2852016
A;Moleculo terror
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S00996
                                                              A;Introns: 17/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                R:Straubinger, B.: Thiebe, R.: Huber, C.: Osterholzer, 1
Biol. Chem. Hoppe-Seyler 369, 601-607, 1988
A:Title: Two unusual human immunoglobulin V-Kappa genes
A:Reference number: S00996; MUID:89134397; PMID:2852016
A:Accession: S10146
F;1-20/Domain: signal sequence #status predicted <br/>
F;21-115/Product: Ig kappa chain V region #status<br/>
F;36-110/Domain: immunoglobulin homology <INM>
                                                                                                                                         A; Note: this sequence was determined C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Homo sapiens (man)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Keywords: heterotetramer; immunoglobulin F;1-19/Domain: signal sequence *status predicted * F;20-114/Product: Ig kappa chain V region *status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Homo sapiens (man)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 23-Jul-1999
                                                                                                                                                              A;Cross-references: EMBL:M27751; NID:g185916; PIDN:AAA58913.1; PID:g185917 A;Note: this sequence was determined from the germline gene
                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-115 <STR>
                                                                                                                                                                                                                                                                                                                                                                    C; Accession: S10146
                                                                                                                                                                                                                                                                                                                                                                                                                                                             S10146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Note: this sequence was determined from the germline gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-114 <STR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Accession: S00996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A:Introns: 11/3; 69/3; 123/2; 173/3; 216/1; 248/1; 279/1; 314/1; 350/3; 430/1; 464/1; C:Superfamily: acetylcholine receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Map position: X
A; Introns: 11/3; 69/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Gene: CESP:C40C9.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Experimental source: C; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Ig kappa chain precursor V region (Al4) - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ig kappa chain precursor V region (AlO) - human (fragment)
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83.3%;
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Pred. No.
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74;
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Query Match
Best Local Similarity 66.7%; Pred. No. 74;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0; .

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Result
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Maximum Match 100%
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    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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   Query
Match
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   SwissProt_40:*
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YGR1_YEAST
NU1M_POLOR
MTF1_SACKL
Y567_HELLPY
CEMA_NEPOL
GAC3_HUMAN
GAC3_MOUSE
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FCG1_HUMAN
EMRD_ECOLI
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DCUA_HELPJ
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PLSC_HAEIN
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(without alignments)
48.025 Million cell updates/sec
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P01658
P87250
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P31442
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Q9v8y7 drosophila
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Hypothetical YyCB. Bacillus sub tilis chu DNA Res. 1:: [2] Caparaman M. "Systematic sub tilis chu DNA Res. 1:: [2] DNA Res. 1:: [2] SEQUENCE FRESTRAIN=168, MEDLINE=980, Kunst F. OA Azevedo V. Borriss R. O. OB Azevedo V. Borritz C., F. Guiseppi G. Denizot F. Choi S.K. O Denizot F. OA Azevedo V. Paritz C., F. Guiseppi G. Denizot F. OA Azevedo V. Parrosecan E. OA OPATROSATO V. Parrosecan E. N. Isateger M. Is Sato T. Scaskiguchi M. Takeuchi M. Takeuchi M. Takeuchi M. Takeuchi M. Tosato V. Wiari A. Wainters P. Yoshida K. Nature 390: "The complet subtilis."; Nature 390: -i-SUBCELLI	B_BACSU YYCB_BACS P37482; P3762; P3762; O1-OCT-11	00000000000000000000000000000000000000
UN-2002 Illus sub llus sub llus sub eria; Fil TraxID=1. TraxID=1. INE=9605 INE=9605 INE=9605 INE=960 INE=9804 I	ACSU 1994	N
cal transport p subtilis. Firmicutes; Ba Firmicutes; Ba D=1423; FROM N.A. 8; 6051385; PubMed N. Nakai S. chromosome cont 1:1-14(1994). FROM N.A. 88804403; PubMed Ogasawara N. 1:1-14(1994). FROM N.A. 8040403; PubMed Ogasawara N. Codani J.J. Codani J.J. Codani J.J. Fujita M., Fuj Codani J.J. Codani J.J. Codani J.J. Fujita M., Fuj Codani J.J. Codani J.J. Levine K.M. D. Errington J Fujita M., Fuj Codani J.J. Codani	(Rel	88888888888888 5888888888888 68888888888
subtilis. FEROM N.A. 68; 96051385; PubMed=75840 96051385; PubMed=75840 a N. Nakai S. yoshikatic sequencing of the chromosome containing 1:1-14(1994). FROM N.A. 68; 903asawara N. Moszer V. Bertero M.G. Bess R. Boursier L. Branss S. Bruschi C.V. Ca Codani J.J. Conner F. Davine K.M. Duste E. Bruschi C.V. Ca Codani J.J. Conner F. Davine K.M. Duste L. Branshi S. Hoso Karamata D. Kasahar S. Koutter P. Koni Levine A. Liu H. M K. Pohl T.M. Ogawa K Pohl T.M. Portetell E. Pujic C. Rocha E Scanlan E. Schleich N. Tamakoshi A. Tan N. Tamakoshi A. Tan N. Uchiyama S. Vanden J. Sebowska A. Serl A. Tacconi E. Takagi M. Tamakoshi A. Tan N. Uchiyama S. Vanden J. Vanden S. Wipat A. Sept A. Taconi E. Takagi M. Tamakoshi A. Tan N. Uchiyama S. Vanden V. Wipat A. Yamamoto N. Yoshikawa H.F. Zu Plice genome sequence P. Wipat A. Vanden V. Wipat A. Vanden V. Yoshikawa H.F. Zu Plice genome sequence	_ ×	467 503 1 575 1 631 1 710 1 711 1 711 1 1541 1 1544 1 1544 1 1544 1 1544 1
es; Baces; Baces	ALIC PRT; ted) sequence	GAC3_RAT LALG6_CAEEL LITR1_SCHPO LYCIG_SCLI LIGA_SALTI LIGAA_SALTI LIGAA_SCO57 LIGAA_ECO57 LIGAA_ECO57 LIGAA_ECO51 LIGAA_ECO5
Illus. Illus. It the Bacillus in."; Borchert S., Borchert S., Darchert S., Carter N.M., J., Daniel R.A., J., Daniel R.A., J., Daniel R.A., J., Carter N.M., Galleron N., Kamano M., Jones L., di M., Klein C., Kumano M., arevic V., edique C., si Noback M., B., Park S.H., Pescott A.M., y M., Reynolds S., Sadaie Y., ffone F., Sadaie Y., rognoni A., rognoni A., rognoni A., assarotti A., assarotti A., egger T., pata K., H., Danchin A., gegger T., Grotential).		P28473 rattus norv Q09226 caenorhabdi Q10286 schizosacch P45848 escherichia P58721 salmonella Q9acp0 salmonella Q9acp0 secherichia Q58720 escherichia P45800 escherichia Q63120 rattus norv Q92887 homo sapien Q28689 oryctolagus Q61879 mus musculu

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RESULT 2
O56A_DROME
                                Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
An Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
An Amanatides P.G., Scherer S.E., Ashburner M., Henderson S.N.,
An George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
An Hoskins R.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
An Hold J., Baybayani A., An H.-J., Andrews Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Ballew R.M., Basu A., Baxendale J., Boyraktaroglu L., Beasley E.M.,
Ballew R.M., Basu A., Barman B.P., Bhandari D., Bolishakov S.,
An Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
Buttis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
An Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
An Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Dietz S.M.,
An Cherry J.M., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
An Posler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
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Best Local
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16-OCT-2001 (Rel. 40, Last
15-JUN-2002 (Rel. 41, Last
Putative odorant receptor 5
OR56A OR CG12501.
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                   Glodek
                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-Berkeley;
MEDLINE-20196006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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InterPro; IPR004747; Cyan_transport.
TIGRFAMS; TIGR00896; CynX; 1.
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6; Conserv
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ilarity 100.0%;
Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=10731132;
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                 Gorrell J.H.,
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Garg N.S., Gelbart W.M., Glasser K., J.H., Gu Z., Guan P., Harrin V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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45C3348FFE2183CD CRC64;
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RA Merkulov G., Milshina N.V., Mobarry C., McDeod M.P., McPherson D.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Rese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Zheng X.H., Zhong F.N., Rubin G.M., Venter J.C.;
"The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).
                                                 Query Match
                                                                                                TRANSMEM
DOMAIN
                                                                                                                                               DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K., Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Tupy J.L., Bergman C.M., Berman B.P., Carlson J.W., Celniker S.E., Clamp M.E., Drysdale R.A., Emmert D., Frise E., de Grey A.D.N.J., Harris N.L., Kronmiller B., Marshall B., Millburn G.H., Richter J., Russo S., Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield B.
                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                             Hypothetical Olfaction; M
                                                                                                                                                                                                                                                                                                                                                       EMBL; AE003794; AAF57517.2; -. FlyBase; FBgn0034473; Or56a. InterPro; IPR004117; 7tm_6.
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between the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Annotation of Drosophila melanogaster genome.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases
-!- EUNCTION: PROBABLE ROLE IN THE ODORANT RESPONSE, BE
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Misra S., Crosby
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Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
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                                                                                 TRANSMEM
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SIMILARITY: BELONGS TO
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                                                                                                                                                                                                                                                                                                                              protein;
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100.0%;
                                                                                                                                                                                                                                                                                                           family.
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CYTOPLASMIC (
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EXTRACELLULAR (POTENTIAL)
7 (POTENTIAL).
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Score 34;
Pred. No.
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PIR; S07485; RNZQ2L.
InterPro; IPR000684; RNA_POLII_repeat.
InterPro; IPR000723; RNA_POL_A.
InterPro; IPR002879; RNA_POL_A; 1.
Pfam; PF00623; RNA_POL_A; 1.
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01-JAN-1990
15-DEC-1998
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                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                   DNA_BIND
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Li W.B., Bzik D.J., Gu H., Tanaka
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Eukaryota; Alveolata;
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                                                                                                                                                                 DNA-binding;
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                                                                                                                                                                                             PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W.B., Bzik D.J., Gu H., Tanaka M., Fox B.A., Inselburg n enlarged largest subunit of Plasmodium falciparum RNA defines conserved and variable RNA polymerase domains.
                                                                                                                                                                                                                                                                                                                                                                                                                        III FOR 5S AND TRNA GENES.
SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TWELVE DIFFERENT POLYPEPTIDES. THIS POLYPEPTIDE IS THE LARGEST COMPONENT OF RNA POLYMERASE II. SUBCELLULAR LOCATION: Nuclear. PTM: THE TANDEM 7 RESIDUES REPEATS CAN BE HIGHLY PHOSPHORYLATED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            {RNA}(N).
SUBUNIT: EACH CLASS OF RNA POLYMERASE IS ASSEMBLED THIS POLYPEPTIDE IS
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CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
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MISCELLANEOUS: THREE DISTINCT ZING-CONTAINING
FOUND IN EURARYOTIC NUCLEI: POLYMERASE I FOR T
PRECURSOR, POLYMERASE II FOR THE MRNA PRECURSO
                                                                                                                          PF00623; RNA_POL_1.

PF01854; RNA_POL_1I_REPEAT; 9.

TE; PS00115; RNA_POL_II_REPEAT; 9.

Sferase; DNA-directed RNA polymerase; Transcription; sferase; DNA-directed: Phosphorylation; Zinc-finge C2H2-TYPE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE
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(Rel. 13, Last sequence update)
(Rel. 37, Last annotation update)
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Apicomplexa;
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6 X TANDEM REPEATS OF [YIV]-D(3,4).
ASP/GLU-RICH (HIGHLY ACIDIC).
ASP/GLU-RICH (HIGHLY ACIDIC).
ASP/GLU-RICH (HIGHLY ACIDIC).
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Haemosporida;
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RESULT 5

KV31_MOUSE
ID KV31_MOUSE
P01661;
71-JUL-198
7-19
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BB19_R
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21-JUL-1986
21-JUL-1986
15-JUL-1999
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Q05005;
Q1-FEB-1994
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TRANSMEM
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SIGNAL 1 21
CHAIN 22 171
                                                                                                                                                                                                                                                   PIR;
                                                                                                                                                                                                                                                                                                  modified and this statement
                                                                                                                                                                                                                                                                                                                                                                       border protein with esterase and phospholipase activity.";
J. Biol. Chem. 268:12901-12911(1993).
-i- SUBCEPLUIDAR LOCATION: Integral membrane protein (Potential).
-i- TISSUE SPECIFICITY: INTESTINE.
-i- DEVELOPMENTAL STAGE: EXPRESSED IN THE INTESTINE OF ADULT BUT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; vertebrata; buv
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oryctolagus cuniculus (Rabbit)
Eukaryota; Metazoa; Chordata; (
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15-JUL-1998
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                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
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171 AA;
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RNAs expressed in intestine of adult but not baby rabbits.
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28, Last sequence up
36, Last annotation
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Blochemistry 17:2392-2400(1978).
[2]
SEQUENCE OF 21-131
                                                                                  21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence up
15-JUL-1999 (Rel. 38, Last annotation
                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00047; ig; 1. SMART; SM00406; IGv; Immunoglobulin V regi
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                                                                                                                                                                                                                                                                                                                                                                                                                                    "Mechanisms of antibody diversity: multiple genes related mouse kappa variable regions."; Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-73140225; PubMed-4691517;
MCKean D.J., Potter M., Hood L.E.;
"Mouse immunoglobulin chains. Pattern of sequence
kappa chains with limited sequence differences.";
 Burstein
          SEQUENCE OF 1-37.
MEDLINE=78235887; PubMed=98179;
                                                                  Mus musculus (Mouse)
                                                                                                                           KV3F_MOUSE
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Mammalia; Eutheria;
                                       NCBI_TaxID=10090;
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Schechter I.;
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Rodentia;
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Rodentia;
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66.7%;
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COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
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                                               Craniata; Ver
Sciurognathi;
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Sciurognathi; Muridae;
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                                                Muridae;
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15-JUL-1998 (Rel. 3
15-JUL-1998 (Rel. 3
30-MAY-2000 (Rel. 3
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-!- FUNCTION: ESSENTÎAL FÓR MITOCHONDRIAL REPLICATION AND TRANSCRIPTION. CONFERS SELECTIVE PROMOTER RECOGNITION SUBJUIT OF THE YEAST MITOCHONDRIAL RNA POLYMERASE. INT DNA IN A NON-SPECIFIC MANNER (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: MITOCHONDRIAL (By Similarity).
-!- SIMILARITY: FAINT SIMILARITY WITH THE T4 GENE 32 PRODUBACTERIAL SIGMA FACTORS.
                                                                                          MEDLINE=97339478;
Carrodeguas J.A.,
"Functional conser
                                                                                                                                         Eukaryota; Fungi; I
Saccharomycetales;
NCBI_TaxID=28985;
                                                                                                                                                    Kluyveromyces lactis (Yeast).
Eukaryota; Fungi; Ascomycota; Saccharo
Saccharomycetales; Saccharomycetaceae;
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HSSP; P01679; 2FBJ.
InterPro; IPR003006;
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MEDLINE=73140224; I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Primary structures of N-terminal extra peptide segments linked the variable and constant regions of immunoglobulin light chain precursors: implications on the organization and controlled expression of immunoglobulin genes.";
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                                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                     6:219-230(1996).
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NEOUS: THE PARTIAL
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17:2392-2400(1978).
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36, Last sequence update)
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                                                                                                    Shadel G.S.,
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21 ONLY IN THE T
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                                                                                                                                                     Saccharomycotina; Saccharomycetes; Setaceae; Kluyveromyces.
                                                                                                                                                                                                                                                          PRT;
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Matches 4
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                                                                                                                                                                                                                                        Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.; "Comparison of whole genome sequences of Chlamydia pneumoniae J1 from Japan and CML029 from USA."; Nucleic Acids Res. 28:2311-2314(2000).

-!- FUNCTION: FIRST STEP OF THE LIPID CYCLE REACTIONS IN THE BIOSYNTHESIS OF THE CELL WALL PEPTIDOCLYCAN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=20330349; PubMed=10871362;
Shirai M., Hirakawa H., Kimoto M., Tab
Shiba T., Ishii K., Hattori M., Kuhara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Read T.D., Brunham R.C., Shen C., Gill S.R., I White O., Hickey E.K., Peterson J., Utterback Linher K., Weidman J., Khouri H., Craven B., I Gwinn M., Nelson W., DeBoy R., Kolonay J., McC Eisen J., Fraser C.M.;
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[2]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MurnAc-pentapeptide phosphotransferase).

MRAY OR CPN0900 OR CP0966.

Chlamydia pneumoniae (Chlamydophila pneumoniae)

Bacteria; Chlamydiales; Chlamyddiaceae; Chlamydo
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Nucleic Acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=20150255; PubMed=10684935;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Genome sequences of Chlamydia trachomatis MoPn and pneumoniae AR39.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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                                                                                                                               CATALYTIC ACTIVITY: UDP-N-acetylmuramoyl-L-alanyl-D-glutamyl-L-lysyl-D-alanyl-D-alanine + undecaprenyl phosphate = UMP + N-acetylmuramoyl-L-alanyl-D-glutamyl-L-lysyl-D-alanyl-D-alanine-
                                                                   diphosphoundecaprenol.
PATHWAY: Peptidoglycan biosynthesis.
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                                         LOCATION:
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66.7%;
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Integral membrane protein (By similarity)
O THE GLYCOSYLTRANSFERASE FAMILY 4. MRAY
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79;
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91 CRC64;
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y K., Bass S.,
, Dodson R.,
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RESULT 9
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P31397;
01-JUL-1993
01-JUL-1993
15-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restructed by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb-
        MEDLINE=21848401; PubMed=11859360; Wood V., Gwilliam R., Rajandream M Sgours J., Peat N., Hayles J., Ba
                                                                                                                                                     Schizosaccharomyces.
NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR003524; PNacPP-
Pfam; PF00953; Glycos_trans;
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                                                                                                      Tanaka K.,
                                                                                                                          STRAIN-ST7
                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                           Schizosaccharomycetales;
                                                                                                                                                                                     Eukaryota;
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                                                                                                                                                                                                         MAP3 OR SPAC3F10.10C.
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TIGR00445; mrax; 1
PS01347; MRAY_1; 1
 Brown D.,
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                                                                      Biol. 13:80-88(1993).
                                                                                                      Davey J.,
                                                                                                                                                                                    Fungi; Ascomycota;
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(Rel. 41, Last annotation
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66.7%;
, Rajandream M.A., Lyne M., Lyne R., Stewart Hayles J., Baker S., Basham D., Bowman S., Brown S., Chillingworth T., Churcher C.M.,
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                                                                                          pombe map3+
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sf_4; 1.
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S -> A (IN REF. 1).
6CAA9283C594A88B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
                                                                                                      Yamamoto M.;
                                                                                                                                                                                     Schizosaccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           division;
                                                                                          encodes
                                                                                                                                                                                               yeast)
                                                                                                                                                                                                                                     update)
                                                                                                                                                                                                                                                                      365
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                                                                                                                                                                                                                                                                                                                                                                          DB
82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transferase; Transmembrane;
                                                                                          the putative M-factor
                                                                                                                                                                                                                                                                                                                                                                                   1; Length 349;
                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           restrictions
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MBL outstation -
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A James K. Jones L. Jones M. Leather S. McDonald S. McLean J. RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C., RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E., RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S., Squares R., Squares R., Squares S., Stevens K., RA Taylor K., Taylor R.G., Tivey A., Walsh S. V., Warren T., Whitehead S., Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B., RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hibert H., Ra Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M., Eger P., Zinmermann W., Wedler H., Wambutt R., Purnelle B., Gallbert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Cadieu E., Dreno S., Gloux S., Lelaure V., Mottier S., Ra Gallbert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Cadieu E., Dreno S., Gloux S., Lelaure V., Mottier S., Dominguez A., Revuelta J.L., Mooreno S., Armstrong J., Forsburg S.L., Shpakovski G.V. Ussery D., Barrell B.G., Nurse P.; The genome sequence of Schizosaccharomyces pombe.";

RL Nature 415:871-880(2002).
D FCG1_HUMAN

D FCG1_HUMAN

C P12314; P12315;

DT 01-CCT-1989 (Rel. 12, Created)

DT 01-CCT-1989 (Rel. 12, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE High affinity immunoglobulin gamma Fc receptor I pre

RI) (FCRI) (IgG Fc receptor I) (CD64).
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FCG1_HUMAN
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                           GNE DT DT ACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Collins M., Connor R., Cronin
Gentles S., Goble A., Hamlin N
Holroyd S., Hornsby T., Howart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send
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                                                                                                                                                                                                                                          294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                THE CELL, NUTRITIONAL CONDITIONS AND PHEROMONE SIGNALING. SIMILARITY: BELONGS TO FAMILY 4 OF G-PROTEIN COUPLED RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: Integral membrane protein.
INDUCTION: BY AT LEAST 3 TYPES OF REGULATION: THE MATING-TYPE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: RECEPTOR FOR THE PEPTIDE PHEROMONE M-FACTOR, A MATING FACTOR OF S.POMBE. PHEROMONE SIGNALING IS ESSENTIAL FOR INITIATION OF MEJOSIS IN S.POMBE; M-FACTOR SIGNALING ALONE MAY BE SUFFICIENT.
                                                                                                                                                                                                                                          LLVWLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A48105; A48105.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the En
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         D10933; BAA01727.1; -. 269369; CAA93308.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pro; IPR001499; STE3_GPCR.
PF02076; STE3; 1.
nembrane; G-protein couple
                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       equires a license agreement (Seemail to license@isb-sib.ch).
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A., Hamlin N., Harris D.,
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100
133
182
283
                                                                                                                                                                                                                                                                                                                    91.2%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                   42498 MW;
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POTENTIAL.
POTENTIAL.
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Pred. No. 85;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
306A022FA7DCFEF7 CRC64;
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                                                                                                                                                                                                                                                                                                               DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pheromone response
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Usage
                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                  Length 365
                                                                           precursor (Fc-gamma
                                                                                                                                                                                                                                                                                                      Indels
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CARBOHYD
CARBOHYD
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DOMAIN
DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                         Pfam; Prove.
SMART; SM00410; IG_ir.
SMART; SM00408; IGc2; 1.
SMART; SM00408; IGc2; 1.
SMART; Receptor; famain; Repeat;
                                                                                                                                                                                                                           DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR;
PIR;
PIR;
PIR;
                                                                                         CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MIM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entre European Bioinformatics Institute. There are no restitute the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A (SHOWN HERE) AND I PRODUCED BY ALTERNATIVE SPLICIMG.
-!- TISSUE SPECIFICITY: MONOCYTE/MACROPHAGE-SPECIFIC:
-!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
-!- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DON-
-!- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DON-
-!- DATABASE: NAME-PROW; NOTE-CD guide CD64 entry;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complementary DNAs.";
Science 243:378-381(1989).
-!- FUNCTION: BINDS TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE=89098339; Allen J.M., Seed B
                    CARBOHYD
                                    CARBOHYD
                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Isolation and expression of functional high-affinity complementary DNAs.":
                                                                                                                                                                                                                                                               TRANSMEM
                                                                                                                                                                                                                                                                                                                                       SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genew; HGNC:3613; FCGR1A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-89100284;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Nucleotide sequence of three cDNAs for the receptor (FCRI).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human)
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; S03018; S03018.
; S03019; S03019.
; A41357; A41357.
; B41357; B41357.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AFFINITY RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   146760;
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X14355; CAA32536.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        IPR003006; Ig_MHC.
IPR003598; Ig_c2.
IPR003600; Ig_like.
                 124
212
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16:11824-11824(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FC
                                                                                     POTENTIAL.

CYTOPLASMIC (POTENTIAL).

IG-LIKE C2-TYPE DOMAIN 1.

IG-LIKE C2-TYPE DOMAIN 3.

IG-LIKE C2-TYPE DOMAIN 3.

BY SIMILARITY.

BY SIMILARITY.
               N-LINKED
                                                     N-LINKED
                                                                                                                                                                                                                                                                            EXTRACELLULAR (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                     Transmembrane; Glycoprotein; Signal; Alternative splicing; Polymorphism.
                                                                                                                                                                                                                                                                                                                  AFFINITY IMMUNOGLOBULIN
               GLCNAC.
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             (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SEQUENCE
                TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                     Burland V.D., Plunkett G. III, Daniels D.L., Blattner F.R.; "DNA sequence and analysis of 136 kilobases of the Escherichia coligenome: organizational symmetry around the origin of replication."; Genomics 16:551-561(1993).
                                         TRANSMEM
                                                           Pfam; PF00083; sugar_tr; 1.
TIGRFAMs; TIGR00880; 2_A_01_02; 1.
                                                                                                                  EcoGene; EG11693;
                                                                                                                               EMBL;
                                                                                                                                         EMBL; L10328; AAA62025.1; ALT_INIT
                                                                                                                                                                                                                                                                                                                   -
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                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "An
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-94059107; PubMed=8240355;
Naroditskaya V., Schloseer M.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Escherichia coli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Multidrug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUL-1993 (Rel. 26,
16-OCT-2001 (Rel. 40,
16-OCT-2001 (Rel. 40,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUL-1993
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                                                   fransport;
                                                                                          InterPro;
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                                                                                                                                                                                                                                                                              SIMILARITY:
AS THE DRUG
                                                                                                                                                                                                                                                                                                                 ENERGY SHOCK ADAPTATIVE RESPONSE. SUBCELLULAR LOCATION: Integral membrane
                                                                                                                                                                                                                                                                                                                                           FUNCTION: MULTIDRUG RESISTANCE PUMP THAT PARTICIPATES IN A LOW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (T)
                                                                                                                                                                                                                                                                   BCR/CMLA SUBFAMILY.
                                                                                                                                                                                                                                                                                                      (Potential).
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                                                                                                                             AE000445;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        tskaya V., Schloseer M.J., Fan N.Y., Lewis coli gene emrD is involved in adaptation tm. Biophys. Res. Commun. 196:803-809(1993).
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                                                                                    IPR004734; Drug_resist.
IPR003662; sub_transporter.
; Transmembrane;
9 29
47 67
74 94
96 · 116
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resistance protein D.
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                                                   Inner membrane;
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BELONGS TO THE
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RESULT 12
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15-JUN-2002 (Rel. 41, Last annotation updath)
High affinity immunoglobulin gamma FC recep
RI) (FCRI) (IGG FC receptor I)
                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
InterPro; IPR003006; Ig_MHC. InterPro; IPR003598; Ig_c2. InterPro; IPR003600; Ig_like. Pfam; PF00047; 1g; 3. SMART; SM00410; IG_like; 2.
                                                                                                        entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                           the European Bioinformatics Institute. Thuse by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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"Molecular cloning and recentor for Tgg ":
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P26151;
                                                 MGD; MGI:95498; Fcgr1.
                                                                                        EMBL; M31314; AAA40056.1; -.
                                                                                                                                                                                                                                                                                                MEDLINE=92166399;
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                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
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                                                                   ; A43511;
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n N., Tate B., McK
ng and expression
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342339DC7265A30B CRC64;
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Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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ion of the mouse high affinity Fc
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RESULT 13
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CARBOHYD
                                                                                                                               This
                                                                                                                                                                                                                                                     Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brow
Smith D.R., Noonan B., Guild B.C., deJonge B.L., C
Tummino P.J., Caruso A., Uria-Nickelsen M., Mills
Gibson R., Merberg D., Mills S.D., Jiang Q., Taylo
   Pfam; PF03605; Dcu; 1.
TIGRFAMs; TIGR00770; Dcu; 1
                         InterPro; IPR004668; Dcu.
                                                                                                       the
                                                                                                                                                                                                  "Genomic sequence comparison of two unrelated gastric pathogen Helicobacter pylori."; Nature 397:176-180(1999).
-I- FUNCTION: RESPONSIBLE FOR THE TRANSPORT OF
                                                                                                                                                                                                                                                                                                                                                        Helicobacter pylori J99 (Campylobacter pylori J99)
Bacteria; Proteobacteria; epsilon subdivision; Hel
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16-OCT-2001 (Rel. 40, Last
16-OCT-2001 (Rel. 40, Last
Anaerobic C4-dicarboxylate
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IgG-binding protein; Rec
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16 LLLWVP 21
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les 4; Conserv
                                                         European Bioinformatics Institute. The by non-profit institutions as long lifted and this statement is not removed. It.es requires a license agreement (See send an email to license@isb-sib.ch).
                                                                                                                                                               THE PERIPLASM ACROSS THE INNER MEMBRANE SUBCELLULAR LOCATION: Integral membrane SIMILARITY: BELONGS TO THE DCUA / DCUB (
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                                                                                                      SWISS-PROT entry is copyright. It is produced through a deen the Swiss Institute of Bioinformatics and the EMBL European Bioinformatics Institute. There are no restrict
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CYTOPLASMIC (POTENTIAL).

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Taylor D.E., Vovis
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RESULT 14
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MEDLINE-97394467; PubMed-9252185;

MEDLINE-97394467; PubMed-9252185;

Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G. Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S., Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S., Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A., McKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K., Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley Cotton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Wal Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
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15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Anaerobic C4-dicarboxylate transporter dcuA.
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                                                                                                                          Nature 388:539-547(1997).
                                                                                                                                     pylori.
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                                                                                                                                                                                                                                                                                                               Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; epsilon subdivision;
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                                                                             FUNCTION: RESPONSIBLE FOR THE TRANSPORT OF THE PERIPLASM ACROSS THE INNER MEMBRANE (BY SUBCELLULAR LOCATION: Integral membrane prosumilarity: Belongs to the DCUA / DCUB (TC
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                SWISS-PROT entry is copyright. It is produced through a collabeen the Swiss Institute of Bioinformatics and the EMBL outst European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in
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                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
                                     PIR; A01900; K3HUVG. HSSP; P80362; 1WTL.
                                                            EMBL; X01668; -; NOT_ANNOTATED_CDS
                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE-85087932;
                                                                                                                                                                                                                                                                 NCBI_TaxID=9606; [1]
                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human)
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13-AUG-1987 (Rel. 05, Last sequence update)
15-UJL-1999 (Rel. 38, Last anotation update)
15 kappa chain V-III region VG precursor (Fragment).
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'Immunoglobulin genes of different subgroups are interdigitated
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O77375 plasmodium
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Mol. Biochem. Parasitol. 111:31-39(2000).
EMBL; AJ271478; CAB70097.1; -.
InterPro; IPR000722; RNA_pol_A.
Pfam; PF00623; RNA_pol_A; 1.
                                                                                                                                                                                                                                                                           Plasmodium yoelii.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5861;
                                                                                                                                                                                                                                                                                                                                     O9NFS8:
01-OCT-2000 (TrEMBLrel. 15, Created)
01-DCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                            SEQUENCE
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Nivez M.P., Achbarou A., Bienvenu J.D., Mazier D., Doerig C.,
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RX MEDLINE-98044033; PubMed-9384377;
RA Azevedo V. Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Fabret C., Ferrari E., Foulger D.,
RA Entlan K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Golighthy E.J., Grandi G.,
RA Gliseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Gliseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Kurita K., Lapidus A., Lardinols S., Lauber J., Lazarevic V.,
RA Kurita K., Lapidus A., Lardinols S., Lauber J., Lazarevic V.,
RA Kurita K., Lapidus A., Lardinols S., Lauber J., Lazarevic V.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Skijuchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Sato T., Sachlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sekuchi M., Tanakoshi A., Tanaka T., Tarahashi H., Takamaru K.,
RA Takeuchi M., Tacconi E., Takagi T., Takahashi H., Takamaru K.,
RA Winters P., Willama S., Vandenbol M., Vannier F., Vassarotti A.,
The Complete genome sequence of the gram-positive bacterium Bacillus
RT Subtilis.", Stata K.,
RA Winters P., Wedlar E., Wedlar E., Yoshikawa H., Danchin A.,
The Complete genome sequence of the gram-posit
                                                                                                      Query Match
Best Local
                                                                                    Matches
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P71055; O08175;
01-FEB-1997 (TrEMBLrel. 0)
01-FEB-1997 (TrEMBLrel. 0)
01-MAR-2002 (TrEMBLrel. 2)
                                                                                                                                                                                          Kunst F., Ogasawara N., Yoshikawa H., Danchin Submitted (NOV-1997) to the EMBL/GenBank/DDBJ EMBL; Z71928; CAA96474.1; -
EMBL; Z94043; CAB98029.1; -
EMBL; Z99121; CAB15436.1; -
                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                STRAIN-168;
                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                       "The complete genome sequence subtilis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fabret C., Quentin Y., Chapal N., Guiseppi A., Haiech J., Denizot F.; Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Fi
Bacillaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacillus subtilis.
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                                                                                                                                                                                Hypothetical
                                                                                                                                                                                                                                                                                                                                                      Nature 390:249-256(1997).
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37 LLIWIP 42
                                             1 LLIWIP 6
                                                                                  Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Firmicutes;
ae; Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (APR-1997)
                                                                                                                                                             11 protein; Complete
367 AA; 42554 MW;
                                                                                    Conservative
                                                                                                    100.0%;
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Last sequence update)
Last annotation updat
                                                                                                Score 34; DB 16;
Pred. No. 1.2e+02;
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88D37986AFD9C9C6
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databases
                                                                                                                                                             CRC64;
                                                                                                                     Length 367;
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                                                                                  0,
                                                                                  Gaps
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RESULT 5
Q9ZQZ2
ID Q9ZQ
AC Q9ZQ
DT 01-M
DT 01-M
DT 01-M
DT 01-M
DT 11-M
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Q8WVN7
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Q92521
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Matches 6
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                     Q9ZQZ2
Q9ZQZ2;
Q1-MAY-1999
Q1-MAY-1999
Q1-MAR-2002
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Q92521;
Q1-FEB-1997
Q1-FEB-1997
Q1-JAN-1999
                                                                                                                                                                                                                                                                                                                                                            OBWVN7
OBWVN7; PRELIMINARY;
O1-MAR-2002 (TrEMBLrel. 20,
O1-MAR-2002 (TrEMBLrel. 20,
O1-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                     Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases EMBL; BC017711; AAH17711.1; ~.
SEQUENCE 554 AA; 64957 MW; E778418C02A27488 CRC64;
                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                    Phosphatidylinositol glycan,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE-97015126; PubMed-8861954;
Takahashi M., Inoue N., Ohishi K., Maeda
Takahashi T., Takeda J., Kinoshita T.;
             Putative LRR
                                                                                                                                                                                                                                                                     TISSUE-PROSTATE;
                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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like protein
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lumenal domain, is involved in transferring the third mannose of the
                                                                                                                               138 LLIWIP 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      138 LLIWIP 143
                                                                                                                                                                           Local Similarity hes 6; Conserv
                                                                                                                                                    1 LLIWIP 6
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                     (TrEMBLrel. 10, TrEMBLrel. 10, CTrEMBLrel. 20,
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                                                                      PRELIMINARY;
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 kinase).
             receptor-linked
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09,
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Last annotation updat,
class B.
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                                                                                                                                                                                      Score 34; DB 4;
Pred. No. 1.8e+02;
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Pred. No. 1.8e+02;
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             (Putative LRR receptor-
                     update)
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank
EMBL; AC005275; AAD14467.1; -.
EMBL; AL161496; CAB77824.1; -.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR0003592; LRR_out.
InterPro; IPR003592; LRR_out.
InterPro; IPR002965; P_rich_extensn.
Pfam; PF00560; LRR; 5.
Pfam; PF00069; pkinase; 1.
PRINTS; PR01217; PRICHEXYENSN.
ProDom; PR000001; Euk_pkinase; 1.
SMART; SM00370; LRR; 4.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
ATP-binding; Kinase; Receptor; Transfera
SEQUENCE 754 AA; 82315 MW; 56E59466A
                          Bowman S., Lawson D., Basham D., Brown D., Chillingworth T., Churcher C.M., Craig A., Davies R.M., Devlin K., Feltwell T., Gentles S., Gwilliam R., Hamlin N., Harris D., Holroyd S., Hornsby Horrocks P., Jagels K., Jassal B., Kyes S., McLean J., Moule S., Mungall K., Murphy L., Oliver K., Quail M.A., Rajandream M.-A., Rutter S., Skelton J., Squares R., Squares S., Sulston J.E., Whitehead S., Woodward J.R., Newbold C., Barrell B.G., Whitehead S., Woodward J.R., Newbold C., Barrell B.G.,
                                                                                                                                                                                                                                                                  01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DNA-directed RNA polymerase II.
                                                                                                                                                                                                                                                                                                              O77375 PRELIMINARY;
O77375;
O1-NOV-1998 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Spiegel L.A., Huang E.N., Nascimento L.U., de la Bastide M., Vil D.M., Preston R.R., Matero A., Shah R., O'Shaughnessy A., Rodriguez M., Shekher M., Schutz K., See L.H., Swaby I., Habermann K., Dedhia N.N., Mewes H.W., Lemcke K., Mayer K.F.X.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F4C21.35 OR AT4G03390.

Arabidopsis thallana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheo; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                       MEDLINE=99376085;
                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                   Plasmodium falciparum 
Eukaryota; Alveolata;
                                                                                                                                                                                                                                                  DNA-directed RNA polymerase PFC0805W, MAL3P6.20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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"Arabidopsis thaliana
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falciparum
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             complete nucleotide sequence
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llarity 100.0%;
Conservative C
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                                                                                                                                       PubMed=10448855;
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Apicomplexa;
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Pred. No. 2.4e+02;
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56E59466A597F63D CRC64;
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              of chromosome
                                                                                                                                                                                                                 Haemosporida; Plasmodium.
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Parnell L.D.,
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              of.
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             Flasmodium
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RESULT 7
Q985W5
 RP OCC OCN DTT DTT ACC
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Q8TTC2
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Best Local
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                                                                                    OBTTC2; PRELIMINARY;
OBTTC2;
01-JUN-2002 (TrEMBLrel. 2
01-JUN-2002 (TrEMBLrel. 2
01-JUN-2002 (TrEMBLrel. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q985W5;
Q985W5;
01-OCT-2001
01-OCT-2001
01-MAR-2002
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InterPro; IPR000722; RNA_pol_A.
InterPro; IPR002879; RNA_pol_A2.
Pfam; PF006.33; RNA_pol_A; 1.
Pfam; PF01854; RNA_pol_A2; 1.
PROSITE; PS00115; RNA_POL_II_REPEAT; UNKNOWN_10.
                                                                                                                                                                                                                                                                                   Hypothetical SEQUENCE 1:
                                                                  Predicted protein. MA0515.
                                                                                                                                                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                                                                                                                                                    Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sase Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsunoto Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimot Takeuchi C., Yamada M., Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rhizobium loti (Mesorhizobium loti).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae
Phyllobacteriaceae; Mesorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein mlr7498. MLR7498.
SEQUENCE FROM N.A.
                                Archaea; Euryarchaeota; Methanosarcinaceae; Metl
                                                      Methanosarcina acetivorans
                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-MAFF303099;
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA-directed RNA polymerase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 400:532-538(1999).
EMBL; Z98551; CAB11131.1;
                                                                                                                                                                                                                                                                                                                      DNA Res.
                                                                                                                                                                                                                                                                                                                                Mesorhizobium loti."
                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=21082930; PubMed=11214968;
                                                                                                                                                                                                                                                                                                                                            "Complete genome structure of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    582
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity 6; Conserv
                                                                                                                                                                                                                                        Similarity 5; Conserv
                                                                                                                                                                                                                                                                                                                      7:331-338(2000).
                                                                                                                                                                                                                                                                                    133 AA; 14309 MW;
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                                 Methanosarcina.
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21,
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                                          Methanococci;
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Last annotation update)
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                                                                                      Last sequence update)
Last annotation update)
                                                                                                              Created)
                                                                                                                                                                                                                                                 Score 33;
Pred. No.
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Pred. No.
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E2C038E77A39DDED CRC64;
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                                                                                                                                                                                                                                                                                                                                           nitrogen-fixing symbiotic bacterium
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                                                                                                                                     290
                                            Methanosarcinales;
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RESULT OF CONTROL OF C
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RA MEDLINE-97313271; PubMed-9169875;

RA Araujo R., Aparicio A., Barrell B., Badcock K., Benes V., Botstein D.,

RA Araujo R., Aparicio A., Barrell B., Badcock K., Benes V., Botstein D.,

Bowman S., Bruckner M., Carpenter J., Cherry J.M., Chung E.,

Churcher C., Coster F., Davis R., Davis R.M., Dietrich F.S.,

Delius H., DiPaolo T., Dubois E., Dusterhoft A., Duncan M., Floeth M.,

Fortin N., Friesen J.D., Fritz C., Goffeau A., Hall J., Hebling U.,

RA Heumann K., Hilbert H., Hillier L., Hunicke-Smith S., Hyman R.,

A Heumann K., Hilbert H., Hillier L., Hunicke-Smith S., Hyman R.,

RA Johnston M., Kalman S., Kleine K., Komp C., Kurdi O., Lashkari D.,

RA Lew H., Lin A., Lin D., Louis E.J., Marathe R., Messenguy F.,

RA Mewes H.W., Mirtipati S., Moestl D., Muller-Auer S., Namath A.,

RA Nentwich U., Oefner P., Pearson D., Petel F.X., Pohl T.M.,

RA Purnelle D., Schafer M., Scharfe M., Scherens B., Schramm S.,

RA Schroeder M., Sdicu A.M., Tettelin H., Urrestarazu L.A., Ushinsky S.,

RA Vierendeels F., Vissers S., Voss H., Walsh S.V., Wambutt R., Wang Y.,

RA Wedler E., Wedler H., Winnett E., Zhong W.W., Zollner A., Vo D.H.,
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RA Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,

RA FitzHugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A.,

RA Allen N., Naylor J., Stange-Thomann N., DeArellano K., Johnson R.,

RA Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,

RA Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,

RA Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,

RA Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,

RA Linton L., McEwan P., McKernan D.E., Grahame D.A., Guss A.M.,

RA Linton L., McEwan P., McKernan D.E., Grahame D.A., Guss A.M.,

RA Linton L., McEwan P., McKernan D.E., Grahame D.A., Guss A.M.,

RA Linton L., McEwan D.E., Krzycki J.A.,

Smith K.,

RA Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,

RA Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,

RA Ferry J.G., Jarrell K.F., Jing H., Mcaraio A.J.L., Paulsen I.,

RA Ferry J.G., Jarrell K.F., Jing H., Mcaraio A.J.L., Paulsen I.,

RA Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,

RA Mctcalf W.W., Birren B.;

RT "The genome of Methanosarcina acetivorans reveals extensive metabolic

RT and physiological diversity.";

Genome Res. 12:532-542(2002).

REMBL: ABBO10712: AAM03959.1; -.
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01-NOV-1996 (TrEMBLrel. 01, C
01-NOV-1996 (TrEMBLrel. 01, L
01-JUN-2002 (TrEMBLrel. 21, L
Chromosome XVI COSMID 9659
YPR147C OR P9659.18
              Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du Z., Favello A., Fulton L., Gattung S., Greco T., Kirsten J., Kucaba Hallsworth K., Hawkins J., Hillier L., Jier M., Johnson D., Johnston L., Langston Y., Latreille P., Le T., Mardis E., Meneze
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
Johnston L.,
                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                Nature 387:0-0(0).
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5; Conserv
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83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                 of Saccharomyces cerevisiae
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Last annotation updat
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Pred. No.
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1.5e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                 chromosome XVI."
                      Menezes S.,
                                                                                                                             Du 2.,
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RESULT 11
Q9KZH9
ID Q9KZH
AC Q9KZH
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Q98K16
ID Q98K1
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Best Local S
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Best Local :
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                                                                                                                                                                                                                                 Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamo Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T. Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A. Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto I. Takeuchi C., Yamada M., Tabata S.;

"Complete genome structure of the nitrogen-fixing symbiotic I.";

Mesorhizobium loti.";

DNA Res. 7:331-338(2000).

EMBL: AP002998: BAB48998.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Q98K16 PRELIMINARY; PRT; 326 AA. Q98K16; 01-CCT-2001 (TrEMBLrel. 18, Created) 01-OCT-2001 (TrEMBLrel. 18, Last sequence update) 01-MAR-2002 (TrEMBLrel. 20, Last annotation update) Permease protein of ribose ABC transporter. MLL1679.
                                                                                                                                                                                                                                                                                                                                                                                                            Rhizobium loti (Mesorhizobium loti).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Phyllobacteriaceae; Mesorhizobium.
                                                                                                                                                                                                           Complete
                                                                                                                                                                                                                                                                                                                                                            STRAIN=MAFF303099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jia Y., Cherry J.M.;
Submitted (SEP-1997) to tl
EMBL; U40829; AAB68285.1;
SGD; S0006351; YPR147C.
                                                                                                                                                                                                                                                                                                                                               MEDLINE=21082930; PubMed=11214968;
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=381;
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InterPro; IPR000379; Ser_estrs_site.
PROSITE; PS00120; LIPASE_SER; UNKNOWN_1.
SEQUENCE 304 AA; 34842 MW; B37EE95D4
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Taich A., Trevaskis E., Vignati D., Wilcox L., Wohldman
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83.3%;
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                                                                                                                                              Score 33; DB 16;
Pred. No. 1.7e+02;
1; Mismatches 0;
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man P., Vaudin
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imura T.,
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Q9KZH9; 01-OCT-2000 01-OCT-2000

(TrEMBLrel.

15, 15,

Created) Last seq

sequence update)

Q9KZH9

PRELIMINARY;

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RESULT
Q936UL
ID 601
ID 609
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RESULT 13
005611
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Q936U1;
01-DEC-2001
01-DEC-2001
01-MAR-2002
 005611;
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                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRALN=LS46-6; TRANSPOSON=TN5046;
MEDLINE=21604134; PubMed=11763242;
MINDAINE=2.7, Kholodii G.Y., Gorlenko Z.M., Minakhina S.V.,
Minakhin L.S., Kalyaeva E.S., Kopteva A.V., Petrova M.A.,
Yurieva O.V., Nikiforov V.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical 19
Pseudomonas sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2).";
Coelicolor A3(2).";
Nature 417:141-147(2002).
EMBL; AL353863; CAB88950.1; -.
                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                               Hypothetical
                                                                                                                                                                                                                         Res. Microbiol. 152:811
EMBL; Y18360; CAC80080.
                                                                                                                                                                                                                                                    " Mercury resistance transposons of Gram-negative environmental
bacteria and their classification.";
                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria.
NCBI_TaxID=306;
                                                                                                                                                                                                                                                                                                                                                                                                           Plasmid pKLH466
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Bentley S.D., Chater K.F.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces. NCBI_TaxID=1902;
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138 AA; 1
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(TrEMBLrel. 20, Last annotation update)
l 15.1 kDa protein.
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               PRELIMINARY;
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                                                                                                                                                    94.1%;
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83.3%;
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Pred. No.
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Pred. No. 1
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Query Match
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Matches 5
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01-OCT-2000
01-MAR-2002
                                             Pfam; PF02517; Abi; 1.
Hypothetical protein; Complete
SEQUENCE 200 AA; 22915 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=KHP41; TRANSPOSON=TN5041;
MEDLINE=97419493; PubMed=9274008;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUL-1997 (TrEMBLrel.
01-JUL-1997 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
                                                                                EMBL; AP001512; BAB05198.1; -. InterPro; IPR003675; Abi.
                                                                                                      "Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtili. Nucleic Acids Res. 28:4317-4331(2000).
                                                                                                                                                   STRAIN-C-125 / JCM 9153;
MEDI.NE-20512582; PubMed-11058132;
Takani H., Nakasone K., Takaki Y., Maeno G., S:
Fuji F., Hirama C., Nakamura Y., Ogasawara N.,
                                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN=C-125 / JCM
                                                                                                                                                                                                                                        Bacillaceae; Bacillus
                                                                                                                                                                                                                                                  Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                Bacillus halodurans
                                                                                                                                                                                                                                                                                      Hypothetical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=KHP41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Host-dependent transposition of Tn5041."; Russ. J. Genet. 36:365-373(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nikiforov V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=KHP41; TRANSPOSON=TN5041;
Kholodii G.Y., Mindlin S.Z., Gor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria.
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         94.1%;
83.3%;
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83.38;
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Score 32; DB
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1; Mismatches
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Last annotation updat
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F793D855F156C62D
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                       DB 16;
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., Kuhara S
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RESULT 15
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AC Q9RKX
AC Q9RKX
AC Q9RKX
AC Q9RKX
DT 01-MA
DT 01-MA
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DE Putat
GN SC014
OS Strep
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Search completed: January Job time : 22.3182 secs
                                                                                                                                                       Query Match
Best Local Similarity 83.3
Matches 5; Conservative
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STRAIN-A3(2) / M.145;

Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,

Bentley S.D., Chater K.D., Harris D.E., Quail M.A., Kleser H.,

Thomson N.R., James K.D., Harris D.E., Quail M.A., Kleser H.,

Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,

Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,

Huang C.-H., Kleser T., Larke L., Murphy L., Oliver K., O'Neil S.,

Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,

Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,

Marren T., Mietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                             Hopwood D.A.;
"Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2).";
Nature 417:141-147(2002).
EMBL; AL133213; CAB61673.1; -
SEQUENCE 230 AA; 23916 MW; 5E87093F7CC1CC26 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptomyces coelicolor.

Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.

NCBI_TaxID-1902;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9RKX7;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Putative integral membrane protein.
SCO1418 OR SC6D7.21C.
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                                                                                                                                                       94.1%; Score 32; DB 16; Length 230;
83.3%; Pred. No. 1.9e+02;
tive 1; Mismatches 0; Indels
                  3, 2003, 15:31:56
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Database :
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1: /cgn2_6/ptodata/1,
2: /ggn2_6/ptodata/1,
3: /cgn2_6/ptodata/1,
4: /cgn2_6/ptodata/1,
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1 LLIWIP 6
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19.615 Million cell updates/sec
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Listing first 45 summaries
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
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GenCore version 5.1.3 (c) 1993 - 2003 Compus
                                  US-08-995-659-16
US-09-320-424-21
US-09-320-424-25
US-09-577-780-16
US-09-577-780-16
US-08-418-35-5
US-08-477-728-21
US-08-477-728-21
US-08-487-200-21
US-08-484-537-21
US-08-484-537-21
US-08-484-537-21
US-08-484-548-6
US-08-484-548-6
US-09-450-520A-6
PCT-US-95-15716-6
US-08-477-728-67
US-08-487-2117D-25
US-08-436-7117-25
US-08-436-717-25
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US-08-162-102C-47	US-08-162-102C-27	US-08-976-288A-66	US-08-129-930B-66	US-07-977-696C-66	US-09-393-627B-28	US-09-532-856-7	US-09-301-593-36	US-08-902-516-2	US-08-653-402B-12	PCT-US93-11611-9	US-08-483-632-2	US-08-483-636-2	US-08-379-057-16	US-08-579-378A-18	US-08-579-378A-14	US-08-484-537-67	US-08-836-561-25
Sequence 47, Appl	`	`	Sequence 66, Appl	•	Sequence 28, Appl	Sequence 7, Appli	Sequence 36, Appl	Sequence 2, Appli	Sequence 12, Appl	Sequence 9, Appli	Sequence 2, Appli	Sequence 2, Appli	`	Sequence 18, Appl	•	`	Sequence 25, Appl

ALIGNMENTS

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; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-996-139-16
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                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:

APPLICATION NUMBER: USSN 60/064,671

FILING DATE: 14 OCTOBER 1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: USSN 08/813,509

FILING DATE: 07 MARCH 1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: USSN 08/772,330

FILING DATE: 23 DECEMBER 1996

ATTORNEY/AGENT INFORMATION:
                                                                                                                                       INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.
SOFTWARE: Microsoft Word for Power Macintosh
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Anderson, Dirk M.
APPLICANT: Galibert, Laurent
APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                           NAME: Perkins, Patricia Anne REGISTRATION NUMBER: 34,693 REFERENCE/DOCKET NUMBER: 2851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 51 Uni
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION:
                                                           amino acid
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                                                                                     20 amino acids
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                                                                                                                                                           (206)233-0644
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JMBER: US/08/996,139
22 DECEMBER 1997
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; TOPOLOGY: linear
; MOLECULE TYPE: prot
US-08-995-659-16
RESULT 3
US-09-215-649A-16
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                                                                                                                              Matches
                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 16, Application US/08995659 Patent No. 6242213 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                          TELEPHONE: (206)587-0430
                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia
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APPLICATION NUMBER: US
FILING DATE: 07 MARCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.
SOFTWARE: Microsoft word for Power Macintosh
CURRENT APPLICATION DATA:
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TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                   11 LLLWVP 16
                                                                                                                                                                                                                                                                                                                                       NAME: Perkins, Patricia REGISTRATION NUMBER: 34, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: 22 DECCLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: USSN 08/772,330 FILING DATE: 23 DECEMBER 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 1 CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
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                                                                                                1 LLIWIP 6
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                                                                                                                              Conservative
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                                                                                                                                                                                                    protein
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14 OCTOBER 1997
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22 DECEMBER 1997
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66.7%;
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CH 1997
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Pred. No.
                                                                                                                                          Score 31; DB Pred. No. 21;
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                                                                                                                              Mismatches
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Macintosh 6.0.1
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US-09-320-424-25
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Best Local S
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
EARLIER APPLICATION NUMBER: 09/048,641 EARLIER FILING DATE: 1998-03-26 EARLIER APPLICATION NUMBER: 08/670,354
                                                              CURRENT APPLICATION NUMBER: US/09/320,424
CURRENT FILING DATE: 1999-05-26
EARLIER APPLICATION NUMBER: 09/190,046
EARLIER FILING DATE: 1998-11-10
                                                                                                                                                         APPLICANT: Wiley, Steven R.
APPLICANT: Goodwin, Raymond G.
TITLE OF INVENTION: Cytokine that Induces Apoptosis
FILE REFERENCE: 2835-E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 16: SEQUENCE CHARACTERISTICS:
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nes 4; Conserv
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REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/215,649A
FILING DATE: 17-Dec-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: USSN 08/772,330 FILING DATE: 23 DECEMBER 1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Anderson, Dirk M. Galibert, Laurent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Receptor Activator of NF-kappaB NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 08/996,139
FILING DATE: CUNKNOWN>
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Perkins,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
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                                                                                                                                                                                                                                                                                              Application US/09320424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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66.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4;
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; EARLIER APPLICATION NUMBER: 09/548,368
; EARLIER FILING DATE: 1995-11-01
; EEARLIER APPLICATION NUMBER: 08/496,632
; EARLIER FILING DATE: 1995-06-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 25
; LENGTH: 20
                                                                              TOPOLOGY: linear;
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ
US-09-577-780-16
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Best Local Similarity
Whiches 4; Conserve
Query Match
Best Local Similarity
Thes 4; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Homo sapiens US-09-320-424-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 16, Application Patent No. 6419929
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 16:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 LLIWIP 6
                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 24-May-2000 CLASSIFICATION: <Unknown> PRIOR APPLICATION DATA:
                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION: NAME: Perkins, Patricia Anne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Maraskovsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 08/995,659
FILING DATE: <UNKNOWN>
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6
                                                                                                                                                                                                                           TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Immunex Corporation, Law Department STREET: 51 University Street
                                                                                                                                                         TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/577,780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Application US/09577780
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                               91.2%;
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66.7%;
              Score 31; DB
Pred. No. 21;
2; Mismatches
                2;
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Pred. No.
                                                                                                      ID NO:
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                                                                                                      16:
                                DB 4;
21;
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                                                 Length 20;
                Indels
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              Gaps
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                                                                                                                                                                                                                                              RESULT 7
US-07-634-278-21
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                                                                                                                                                                                                    Sequence 21, APP--
Sequence 21, APP--
Sequence 21, APP--
                                                                                                                                                                                         Patent No. 5530101
GENERAL INFORMATION:
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APPLICANT: CHESTNUT, JONATHAN
APPLICANT: HOEFFLER, JAMES P.
TITLE OF INVENTION: NOVEL SYS'
TITLE OF INVENTION: IDENTIFYI
TITLE OF INVENTION: VECTORS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (516) 742-43
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: DIGICLIO, FRANK S.
REGISTRATION NUMBER: 31,346
REFERRNCE/DOCKET NUMBER: 1109
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, S
                                                                                                                                      APPLICANT: QUEEN, Cary L. APPLICANT: CO, Man Sung APPLICANT: SCHNEIDER, Wil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                CORRESPONDENCE ADDRESS:
                                                                     APPLICANT: SELICK, Harold E
                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/518,835 FILING DATE: 24-AUG-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                   11 LLLWVP 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: GARDEN CITY STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
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                   ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                  1 LLIWIP 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 21 amino acids amino acid
                                                                                                                                                                                                                             Application US/07634278
                                                                                                   CO, Man Sung
SCHNEIDER, William P.
LANDOLFI, Nicholas F.
COELINGH, Kathleen L.
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379 Lytton Avenue
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                Townsend and Townsend Khourie and Crew
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1 742-4366
NO: 5:
                                                                   IMPROVED HUMANIZED IMMUNOGLOBLINS
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                                                    113
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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22;
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COUNTRY:

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Best Local Similarity
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APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-00266
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INFORMATION FOR SEQ ID NO: :
SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        equence 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                               ENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tent No.
                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                         APPLICANT: QUEEN, Cary L.
APPLICANT: SCHNEIDER, William P.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUM
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
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CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: US 07/590,274
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PM PC COMPATION
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
APPLICATION NUMBER: US/07/634,278
                                                                                     CURRENT APPLICATION DATA:
PRIOR APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (415) 326-2400
                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                 ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: Palo Alto
                                                   APPLICATION NUMBER: US/08/477,728 FILING DATE: 07-JUN-1995
                                                                                                                                                                                                            COUNTRY: US CZIP: 94111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 LLLWVP 16
                                                                                                                                                                                                                                                     STATE:
                                CLASSIFICATION:
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                                                 07-JUN-1995
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19-DEC-1990
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Pred. No. 1.2e+02;
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-477-728-21
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (415) 325-24.
INFORMATION FOR SEQ ID NO:
            APPLICATION NUMBER: US 0: FILING DATE: 28-SEP-1990 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 0: FILING DATE: 13-FEB-1989
                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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LENGTH: 126 amino acid
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APPLICATION NUMBER:
FILING DATE: 28-SEP-
                                                                                                                                   PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION: NAME: Smith, William M
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  FITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                  APPLICATION NUMBER: US/08/474,040 FILING DATE: 07-JUN-1995 CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
STREET: 3
                                                                                              APPLICATION NUMBER: US 07
                                                                                                                                                                                                                                                                                                           COUNTRY: UZIP: 94301
                                                                                                                                                                                                                                                                                                                                           CITY: Palo Alto
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                             379 Lytton Avenue
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LANDOLFI, Nicholas F.
COELINGH, Kathleen L.
SELICK usperson
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SCHNEIDER, William
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28-DEC-1988
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66.7%;
                                                                                                                 US 07/634,278
                                                                                 us 07/590,274
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; Pred. No. 1.2e-
2; Mismatches
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US-08-487-200-21
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APPLICANT: QUEEN, Cary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 10
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TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 7-JUN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
NUMBER OF SEQUENCES: 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY_AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002610
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: J, STREET: J, Palo Alto
                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                   APPLICATION NUMBER: US 0' FILING DATE: 28-SEP-1990
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TYPE: amino acid
                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 LLLWVP 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 LLIWIP 6
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28-DEC-1988
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66.7%;
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Pred. No. 1
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                                                                                                                                         ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-656-586-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: protein US-08-487-200-21
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INFORMATION FOR SEO ID NO: 21
SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6, Application US/08656586 Patent No. 5834597 GENERAL INFORMATION:
                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Liebeschuetz, Joseph O.
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 1182:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: TWO LINE CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Tso, J. Yun
APPLICANT: Cole, Michael S.
APPLICANT: Cole, Michael S.
APPLICANT: Anasetti, Claudio
TITLE OF INVENTION: Mutated No. 5834597activating IgG2 Domains and
TITLE OF INVENTION: Anti-CD3 Antibodies Incorporating the Same
                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/0 FILING DATE: 31-MAY-1996
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11 LLLWVP 16
                                                                                                                                                                                               TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                   1 LLIWIP 6
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                                                                                                                                                                                           amino acid
                                                                      Conservative
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66.7%;
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                                                                   Score 31; DB 2;
Pred. No. 1.2e+02;
2; Mismatches (
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Pred. No. 1.2e+02;
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                                                                                                    Length 126;
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                                                                   Indels
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                                                                   Gaps
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RESULT 12 US-08-484-537-21 ; Sequence 21, Application US/08484537 ; Patent No. 6180370

GENERAL INFORMATION:

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RESULT 13
US-08-649-100-33
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                                                                                                                                        Patent No. 6114507
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 28-SEP-1990

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REGERENCE/DOCKET NUMBER: 11823-00260
                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: protein 08-484-537-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO:
            APPLICANT: SHIRAKAWA, KAMON
APPLICANT: MATUSUE, TOWOKAZU
APPLICANT: NAGATA, SHIGEKAZU
APPLICANT: CO, MAN SUNG
APPLICANT: VASQUEZ, MAXIMILIANO
TITLE OF INVENTION: ANTI-FAS LIGAND ANTIBODY AND ASSAY
TITLE OF INVENTION: METHOD USING THE ANTI-FAS LIGAND ANTIBODY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS: Townsend and Townsend Khourie and Crew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                     11 LLLWVP 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/07/634,278 FILING DATE: 19-DEC-1990 APPLICATION NUMBER: US 07/590,274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
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                                                                                                                                                                                                                                                                                                        1 LLIWIP 6
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                                                                                                                                                            3, Application US/08649100 6114507
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: California
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CO, Man Sung
SCHNEIDER, William P.
LANDOLFI, Nicholas F.
COELINGH, Kathleen L.
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Pred. No. 1
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.2e+02;
0;
                                                                                                                                                                                                                                                                                                                                                                          Length 126;
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RESULT 14
US-08-348-548-6
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; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-649-100-33
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/348,548
FILING DATE: 01-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 06132/009001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617),542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No. 02301.

Patent No. 02301.

GENERAL INFORMATION:

APPLICANT: Berdoz, Jose

APPLICANT: Kraehenbuhl, Jean Pierre

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Best Local :
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INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 127 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street, Suite 3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR, GERALD M
REGISTRATION NUMBER: 28,977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: PO BOX 747
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COUNTRY: USA
TTD: 22040-0747
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CITY: B
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CITY: FALLS CHURCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 02110-2804
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Pred. No. 1.2e+02;
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APPLICANT: Vasquez, Maximiliano
APPLICANT: Landolfi, Nicholas F.
APPLICANT: Candolfi, Nicholas F.
APPLICANT: Tsurushita, Nacya
APPLICANT: Queen, Cary L.
APPLICANT: Queen, Cary L.
TITLE OF INVENTION: Humanized Antibodies To Gamma-Interferon
FILE REFERENCE: 011823-008110US
CURRENT APPLICATION NUMBER: US/09/450,520A
CURRENT FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: 60/110,523
PRIOR FILING DATE: 1998-12-01
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
LENGTH: 128
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:human-mouse
OTHER INFORMATION: transgenic construct HuZAF VL
US-09-450-520A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TELEX: 200154
; INFORMATION FOR SEO ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: '128 amino acids
TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-348-548-6
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Search completed: January 3, 2003, 15:34:27 Job time: 10 secs
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Best Local Similarity 66.7%;
Matches 4; Conservative
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Rest Local Similarity 66.;
atches 4; Conservative
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09-450-520A-6
Sequence 6, Application US/09450520A
Patent No. 6329511
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66.7%;
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                                                                                                                                                            0;
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Minimum
Maximum
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Perfect score:
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DB seq
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length: 2000000000
          US-09-543-188A-3
34
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                                                                                                                                                                                                                                                                                                                            Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                        Published_Applications_AA: *
/cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
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0: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
0: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
0: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
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23.825 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

18 19	17	16	15	14	13	12	11	10	9	8	7	ď	ഗ	4	ω	N	1	Result No. Sc
<u>υ</u> μ	31	31	<u>3</u>	31	31	31	31	31	31	31	31	31	31	31	31	32	34	Score
91.2	91.2	91.2	91.2	91.2	91.2	91.2	91.2	91.2	91.2	91.2	91.2	91.2	91.2	91.2	91.2	94.1	100.0	Query Match
147	144	134	132	131	130	128	128	123	107	107	106	98	80	20	20	177	87	Length
10	10	10	9	10	10	10	10	10	10	10	10	10	10	10	9	10	10	DB
US-09-894-018-131	US-09-894-018-129	US-09-881-823-2	US-09-879-461-2	US-09-286-240-2	US-09-894-018-99	US-09-992-524-6	US-09-881-823-14	US-09-894-018-109	US-09-894-018-103	US-09-894-018-93	US-09-894-018-95	US-09-894-018-101	US-09-894-018-97	US-09-871-856-16	US-09-877-650-16	US-09-764-864-942	US-09-864-761-40310	ID
Sequence 131, App	Sequence 129, App	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 99, Appl	Sequence 6, Appli	14, 1	109,	103,	93,	Sequence 95, Appl	Sequence 101, App		Sequence 16, Appl	Sequence 16, Appl	Sequence 942, App	Sequence 40310, A	Description

ALIGNMENTS

RESULT 1 US-09-864-761-40310

Sequence 40310, Application US/09864761 Patent No. US20020048763A1

GENERAL INFORMATION:

APPLICANT:

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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: DCT/US01/00664
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
DBIOD FILING DATE: 2001-11-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                  PRIOR
PRIOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: Aeomica-X-1
                                                    PRIOR
                                                                                                      APPLICATION NUMBER: PCT/US01/00668
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00663
FILING DATE: 2001-01-30
                                                                                                                                                                                                                         APPLICATION NUMBER: PCT/US01/00665 FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00662 FILING DATE: 2001-01-30 APPLICATION NUMBER: PCT/US01/00661 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Penn, Sharron G.
Rank, David R.
Hanzel, David K.
Chen, Wensheng
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RESULT 3
US-09-877-650-16
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Best Local Similarity
Standard 5; Conservat
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-864-942
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Best Local Similarity
""" hes 6; Conserve
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                                                                                                  Sequence 16, Application US/09877650 Patent No. US20020169117A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 942, Application US/09764864 Patent No. US20020132753A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 40310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: E
OTHER INFORMATION: E
OTHER INFORMATION: E
OTHER INFORMATION: E
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NUMBER OF SEQ ID NOS: 1792
OFTWARE: PatentIn Ver. 2.0
O ID NO 942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/764,864 CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PTZ23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 87
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                                                                                                                                                                                                                                                           35 LLLWIP 40
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APPLICANT: Anderson, Dirk M.
Galibert, Laurent
Maraskovsky, Eugene
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: PCT/US01/00670 FILING DATE: 2001-01-30 APPLICATION NUMBER: US 60/234,687 FILING DATE: 2000-09-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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NN. EXPRESSED IN PLACENTA, SIGNAL = 1.3

NN. EXPRESSED IN FETAL LIVER, SIGNAL = 1.1

NN. EXPRESSED IN BONE MARROW, SIGNAL = 1.1

NN. EXPRESSED IN BOULT LIVER, SIGNAL = 1.5

NN. EXPRESSED IN HEART, SIGNAL = 1.2

NN. EXPRESSED IN HEART, SIGNAL = 1.3

NN. EXPRESSED IN BRAIN, SIGNAL = 1.3
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Pred. No.
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Pred. No. 16;
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                                                                                                                                                                                                                                                                                                                                                                                         Length 177;
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US-09-871-856-16
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                                                                                                                                                                                                                                                                                                                                                                                             Sequence 16, Application US/09871856 Patent No. US20020081720A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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11 LLLWVP 16
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OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/877,650
FILING DATE: 08-Jun-2001
CLASSIFICATION: <UNknown>
                 COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.
SOFTWARE: Microsoft Word for Power Macintos
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/995,659
EILING DATE: 1997-12-22
APPLICATION NUMBER: USSN 08/813,509
EILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                       Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Anderson, Dirk M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patrici
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                      CITY: Seattle
STATE: WA
                                                                                                                                                                                                                             ADDRESSEE: Immunex Corporati
STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Perkins, Patricia Anne REGISTRATION NUMBER: 34,693
                                                                                                                                             ZIP: 98101
                                                                                                                                                                COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: WA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Immunex Corporation, Law Department STREET: 51 University Street
APPLICATION NUMBER: US/09/871,856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                   Immunex Corporation,
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Pred. No. 13;
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PRIOR APPLICATION DATA:

FILING DATE: 31-May-2001 CLASSIFICATION: <Unknown>

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APPLICANT: Newman, Mark
APPLICANT: Brown, David
TITLE OF INVENTION: METODS AND SYSTEM FOR OPTIMIZING
TITLE OF INVENTION: MINIGENES AND PEPTIDES THEREBY
FILE REFERENCE: 39963-20033.00
CURRENT APPLICATION NUMBER: US/09/894,018
CURRENT FILING DATE: 2001-06-27
PRIOR APPLICATION NUMBER: PCT/US00/35568
PRIOR APPLICATION NUMBER: US 60/173,390
PRIOR APPLICATION NUMBER: US 60/173,390
PRIOR FILING DATE: 1999-12-28
PRIOR FILING DATE: 1999-12-28
PRIOR APPLICATION NUMBER: US 60/284,221
QΥ
                                                                                                       ; OTHER INFORMATION: HCV.3s2(-3) US-09-894-018-97
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                                                                                                                                                                          NUMBER OF SEQ ID NOS: 368
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 97
LENGTH: 80
TYPE: PRT
                                                 Query Match
Best Local Similarity
                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 97, Application US/09894018 Patent No. US20020119127A1
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                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 2001-04-16
                                                                                                                                          FEATURE:
                                                                                                                                                       ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (206)587-0430
TELEPAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
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 1 LLIWIP 6
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NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206,587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 16:
                                   4;
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FILING DATE: <Unknown>
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
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                                   Conservative
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66.7%;
                                                 91.2%;
66.7%;
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Pred. No. 1
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                                                 Score 31;
Pred. No.
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                                   Mismatches
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                                 0;
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TITLE OF INVENTION: METODS AND SYSTEM FOR OPTIMIZING
TITLE OF INVENTION: MINIGENES AND PEPTIDES THEREBY
FILE REFERENCE: 39963-20033.00
CURRENT APPLICATION NUMBER: US/09/894,018
CURRENT FILING DATE: 2001-06-27
PRIOR APPLICATION NUMBER: PCT/US00/35568
PRIOR FILING DATE: 2000-12-28
PRIOR FILING DATE: 2000-12-28
PRIOR APPLICATION NUMBER: US 60/173,390
PRIOR FILING DATE: 1999-12-28
PRIOR APPLICATION NUMBER: US 60/284,221
PRIOR FILING DATE: 2001-04-16
NUMBER OF SEQ ID NOS: 368
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 95
LENGTH: 106
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CURRENT APPLICATION NUMBER: US/09/894,018

CURRENT FILING DATE: 2001-06-27

PRIOR APPLICATION NUMBER: PCT/US00/35568

PRIOR FILING DATE: 2000-12-28

PRIOR APPLICATION NUMBER: US 60/173,390

PRIOR APPLICATION NUMBER: US 60/284,221

PRIOR FILING DATE: 1999-12-28

PRIOR APPLICATION NUMBER: US 60/284,221

PRIOR FILING DATE: 2001-04-16
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 101
LENGTH: 98
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 66. Matches 4; Conservative
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: EPIMMUNE, Inc.
APPLICANT: Sette, Alessandro
APPLICANT: Chestnut, Robert
APPLICANT: Livingston, Brian
APPLICANT: Baker, Denisw
                                                                                                                                                                                                                                                                                                                              APPLICANT: Baker, Denisw
APPLICANT: Newman, Mark
APPLICANT: Brown, David
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: HCV.PC3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13 LLLWVP 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13 LLLWVP 18
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Brown, David
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66.7%;
                                                                                                                                                                                                                                                                                                                                                                                             Brian
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TITLE OF INVENTION: METODS AND SYSTEM FOR OPTIMIZING TITLE OF INVENTION: MINIGENES AND PEPTIDES THEREBY FILE REFERENCE: 39963-20033.00

CURRENT APPLICATION NUMBER: US/09/894,018

CURRENT FILING DATE: 2001-06-27

PRIOR APPLICATION NUMBER: PCT/US00/35568

PRIOR FILING DATE: 2000-12-28

PRIOR FILING DATE: 1200-12-28

PRIOR APPLICATION NUMBER: US 60/173,390

PRIOR FILING DATE: 1999-12-28

PRIOR APPLICATION NUMBER: US 60/284,221

PRIOR FILING DATE: 2001-04-16

NUMBER OF SEQ ID NOS: 368

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 93

LENGTH: 107
                                                                                                                                                                                                                                                                                                                                                                В
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                                                                                                                                                                                                                                                                                                        RESULT 9
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US-09-894-018-93
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US-09-894-018-95
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                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                     APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                 Sequence 103, Application US/09894018 Patent No. US20020119127A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 93, Application US/09894018 Patent No. US20020119127A1
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Best Local 9
APPLICANT: Livingston, Brian
APPLICANT: Baker, Denisw
APPLICANT: Newman, Mark
APPLICANT: Newman, Mark
APPLICANT: Newman, David
TITLE OF INVENTION: METODS AND SYSTEM FOR OPTIMIZING
TITLE OF INVENTION: MINIGENES AND PEPTIDES THEREBY
FILE REFERENCE: 39963-20033.00
CURRENT APPLICATION NUMBER: US/09/894,018
CURRENT FILING DATE: 2001-06-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ost Local Similarity
                                                                                                                                                                                                         APPLICANT: EPIMMUNE, Inc.
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APPLICANT: Sette, Alessa
APPLICANT: Chestnut, Rob
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Newman, Mark
Brown, David
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Chestnut, Robert
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66.7%;
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Pred. No.
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 10; Length 107; 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                     US-09-881-823-14
; Sequence 14, Application US/09881823
; Patent No. US20020068066A1
; GENERAL INFORMATION:
                                                                                              RESULT 11
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APPLICANT: Baker, Denisw
APPLICANT: Newman, Mark
APPLICANT: Newman, Mark
APPLICANT: Brown, David
TITLE OF INVENTION: METODS AND SYSTEM FOR OPTIMIZING
TITLE OF INVENTION: MINIGENES AND PEPTIDES THEREBY
FILE REFERENCE: 39963-20033.00
CURRENT APPLICATION UNMBER: US(709/894,018
CURRENT FILING DATE: 2001-06-27
PRIOR APPLICATION NUMBER: PCT/US00/35568
PRIOR FILING DATE: 2000-12-28
PRIOR APPLICATION NUMBER: US 60/173,390
PRIOR FILING DATE: 1999-12-28
PRIOR APPLICATION NUMBER: US 60/284,221
В
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                                                                                                                                                  ; OTHER INFORMATION: AOSI.K US-09-894-018-109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 103
LENGTH: 107
TYPE: PRT
                                                                          Best Loc
Matches
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 109
LENGTH: 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 4; Conserv
                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: EPIMMUNE, Inc.
APPLICANT: Sette, Alessandro
APPLICANT: Chestnut, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: PCT/US00/35568 PRIOR FILING DATE: 2000-12-28 PRIOR APPLICATION NUMBER: US 60/173,390 PRIOR FILING DATE: 1999-12-28 PRIOR APPLICATION NUMBER: US 60/284,221 PRIOR FILING DATE: 2001-04-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Livingston, Brian APPLICANT: Baker, Denisw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 368
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 2001-04-16
                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                         FEATURE:
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13 LLLWVP 18
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                                                                                       Local Similarity
                                     1 LLIWIP 6
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                                                                          Conservative
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                                                                                         91.2%;
66.7%;
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                                                                                       Score 31;
Pred. No.
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Pred. No.
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59;
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67;
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; LENGTH: 128
; TYPE: PRT
; ORGANISM: Murine
US-09-881-823-14
                                                                                                                    RESULT 13
US-09-894-018-99
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OTHER INFORMATION:
US-09-992-524-6
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                                                            GENERAL INFORMATION:
                                                                              Sequence 99, Application US/09894018 Patent No. US20020119127A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 07/378,577
PRIOR FILING DATE: 1999-08-20
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn version 3.0
SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6, Application US/09992524 Patent No. US20020091240A1
                                                                                                                                                                                                                                                                                  Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Queen, Cary L.

APPLICANT: Protein Design Labs, Inc.

TITLE OF INVENTION: Humanized Antibodies To Gamma-Interferon
FILE REFERENCE: 011823-008110US
  APPLICANT: EPIMMUNE, Inc.
APPLICANT: Sette, Alessa
APPLICANT: Chestnut, Rob
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SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/992,524
CURRENT FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: 09/450,520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 1999-11-29
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APPLICANT: CHEN, LI
TITLE OF INVENTION: Method for the Treatment and Prevention of Dental Caries
FILE REFERENCE: 22851-032
                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 128
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
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les 4; Conserv
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Sette, Alessandro
Chestnut, Robert
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                                                                                                                                                                                                                                                                                                     91.2%;
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66.7%;
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69;
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APPLICANT: Brown, David

TITLE OF INVENTION: METODS AND SYSTEM FOR OPTIMIZING

TITLE OF INVENTION: MINIGENES AND PEPTIDES THEREBY

FILE REFERENCE: 39963-20033.00

CURRENT APPLICATION UMBER: US/09/894,018

CURRENT FILING DATE: 2001-06-27

PRIOR APPLICATION NUMBER: PCT/US00/35568

PRIOR FILING DATE: 2000-12-28

PRIOR FILING DATE: 2000-12-28

PRIOR APPLICATION NUMBER: US 60/173,390

PRIOR APPLICATION NUMBER: US 60/173,390

PRIOR FILING DATE: 1999-12-28

PRIOR FILING DATE: 2001-04-16

PRIOR FILING DATE: 2001-04-16

NUMBER: OS 60/284,221

PRIOR FILING DATE: 2001-04-16
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US-09-879-461-2
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US-09-286-240-2
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; OTHER INFORMATION: HCV.3s3
US-09-894-018-99
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SEQ ID NO 99
LENGTH: 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Fett, James W
TITLE OF INVENTION: Chimeric and Humanized Antibodies to Angiogenin
FILE REFERENCE: 10498/74073
                                                                                                                                                       Sequence 2, Application US/09879461 Publication No. US20020193575A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 2
LENGTH: 131
TYPE: PRT
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 4; Conserv
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/286,240
CURRENT FILING DATE: 1999-04-05
NUMBER OF SEQ ID NOS: 25
                                               GENERAL INFORMATION:
APPLICANT: Holmes, Stephen D.
APPLICANT: Holmes, Stephen D.
Sylvester, Daniel R.
Sylvester, Daniel R.
TITLE OF INVENTION: Recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
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                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                             4.
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Newman, Mark
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66.7%;
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                                   Recombinant IL4 .
Treatment of IL4
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Pred. No.
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Pred. No.
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Mismatches

70; 10;

Length 130; Indels

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Gaps

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SmithKline Beecham Corporation

IL4 Antibodies Useful in

Mismatches

DB 10; 70;

Length 131;

0;

Gaps

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STREET: Corporate Intellectual Property, UW2220 - 709

Swedeland Rd.

CITY: King of Prussia
STATE: PA

COUNTRY: USA

ZENTRY: PA

COUNTRY: USA

ZENTRY: PA

COUNTRY: USA

COUNTRY: USA

ZENTRY: PA

COUNTRY: USA

COUNTRY: USA

COUNTRY: USA

COUNTRY: LIMP COORDAILS

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER READABLE FORM:

MEDIUM TYPE: SPECENT NOWABER: US/09/879,461

FILING DATE: CONTROL PA

APPLICATION NUMBER: US/09/879,461

FILING DATE: 14-OCT-1993

ATTORNEY/AGENT INFORMATION:

TELEPHONE: C1215) 270-5024

TELEPHONE: C125) 270-5024

TELEPHONE: S10 NO: 2:

SEQUENCE CIARACTERISTICS:

SEQUENCE CIARACTERISTICS:

SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-09-879-461-2

US-09-879-461-2

US-09-879-461-3

GARNEY/AGENT NO. 21:

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Search completed: January 3, 2003, 15:52:04 Job time : 4.77273 secs
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11 LLLWVP 16
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Minimum DB
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Perfect score:
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         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /SIDS2/gcgdata/g
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19: /SIDS2/gcgdata/
20: /SIDS2/gcgdata/
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length: 2000000000
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44
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       SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1988.DAT:

**(SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1988.DAT:*

**(SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT:*

**(SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT:*

**(SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT:*

**(SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1992.DAT:*

**(SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT:*

**(SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT:*

**(SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT:*

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**(SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*

**(SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*

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**(SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:*

**(SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:*

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**(SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:*
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Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA:1986.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA:1987.DAT:*
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                         AAU11827
ABB89811
AAM964792
AAM40205
ABG30232
AAU32016
ABB67564
AAU00427
                                                                                                                                                                                                                                                                                                                          SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Search time 26.5909 Seconds (without alignments) 30.067 Million cell updates/sec
Human polypeptide
Human polypeptide
Novel human diagno
Novel human secret
Drosophila melanog
Caenorhabditis ele
Caenorhabditis ele
                                                                                                                                                                                                                                                      Description
                                                                                                                                                               Human
                                                                                                                                                                                  Peptide ligand for Human polypeptide
                                                                                                                                                               reproductive
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Propionibacterium	AAU43406		160	77.3	34	
Novel human diagno	ABG01550	22	130		34	
Human EST encoded	AAM24385		103	•	34	
Propionibacterium	AAU50181		76		34	
Novel human diagno	ABG01631		62		34	
Interleukin 1 anta	ABB72639		17	٠	34	
ij	AAB17743		17	•	34	
rleukin-1 ty	AAY09966		17		34	
	AAW58320		17	77.3	34	
binding	AAW68833		17		34	
Peptide containing	AAW16194		17	•	34	
Human platelet gly	AAW32770		10	•	34	
Novel human secret	AAU33181		533	•	3 5	
Neisseria meningit	AAY74306		524	•	35	
E. coli cellular p	AAU34459		475		35	
Human G-protein co	ABB76184		382		35	
Haemophilus influe	AAU35593		360		35	
Novel human diagno	ABG10973		195	•	35	
`	AAM89871		117	•	35	
Human signal pepti	AAY87271		109		35	
	ABG37801		83		35	
Human ORF623 prote	ABP31650		54	•	35	
Listeria monocytog	ABB47832		719	•	36	
Propionibacterium	AAU46431		331	•	36	
type 3 inos	AAR99850		2701	•	37	
	AAM93820		836		37	
Protein involved i	AAW14440		561	84.1	37	
Listeria monocytog	ABB49843		461	84.1	37	
Streptococcus poly	ABP30101		458	84.1	37	
Human NOV8 protein	AAU91293		415	84.1	37	
ece.	AAR14114		415	84.1	37	
Group B Streptococ	37		393	84.1	37	
ophila mel	607		385	84.1	37	
tococcus p	æ	23	384	84.1	37	
Human secreted pro	AAU01575	22	27	84.1	37	

ALIGNMENTS

RESULT 1 AAU11827

AAU11827 standard; peptide; 6

AA.

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Prion protein; Prp; ligand; octapeptide motif; scrapie; prion-associated disease; Creutzfeldt-Jakob disease; Gerstmann-Straussler-Scheinker disease; fatal familial insomnia; feline spongiform encephalopathy; bovine spongiform encephalopathy; transmissible mink encephalopathy; exotic ungulate encephalopathy;
        WPI; 2002-061944/08
                              Hammond DJ, Wiltshire VR,
                                                                       05-APR-2000; 2000US-0543188
                                                                                                                                         WO200177687-A2
                                                                                                                                                                                    chronic wasting disease
                                                                                                                                                                                                                                                                                       26-MAR-2002
                                                                                                                                                                                                                                                                                                             AAU11827;
                                                                                              05-APR-2001; 2001WO-US11150
                                                                                                                    18-OCT-2001
                                                                                                                                                                Synthetic
                                                                                                                                                                                                                                                               Peptide ligand for Prion protein, PrP,
                                                    ٧I
                                                    TECHNOLOGIES
                                                                                                                                                                                                                                                                                     (first entry)
                              Carbonell R,
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RESULT 2
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Best Local Similarity
Thes 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                             Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antilinfammatory; antiucer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disord neurological disease; infection; human; secreted protein.
The invention relates to novel genes (ABL89449-ABL90853) and proteins
                                   Claim 11;
                                                                    disorders
                                                                                Novel 1405 isolated polypeptides, useful for diagnosis, treatment and prevention of neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal and proliferative
                                                                                                                                                    N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                     WO200190304-A2
                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human polypeptide SEQ ID NO 2187.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB89811;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New ligands for prion proteins, useful for detection or removal or prions and for treating prion-associated diseases, recognize a spec
                                                                                                                                                                                                                                   (HUMA-) HUMAN GENOME
                                                                                                                                                                                                                                                                  19-MAY-2000; 2000US-205515P
                                                                                                                                                                                                                                                                                                  18-MAY-2001; 2001WO-US16450
                                                                                                                                                                                                                                                                                                                                   29-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 16; Page 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               octapeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 WLYWIP 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  invention relates to
                                                                                                                                                   2002-122018/16
DB; ABL90220.
                                                                                                                                                                                                    CE,
                                   SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    for treating prion-associated diseases, recognize a specific
                                                                                                                                                                                                  Rosen CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   motif
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,
                                ID NO 2187; 2081pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               is a ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 44; DB 25;
Pred. No. 7.8e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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RESULT 3
AAM96472
ID AAM9
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Best Local
                                                                               14-JUL-2000;
26-JUL-2000;
26-JUL-2000;
14-AUG-2000;
                                                                                                                                                                                                                              28-JUN-2000;
30-JUN-2000;
07-JUL-2000;
                                                                                                                                                                                                                                                                                         18-APR-2000;
19-MAY-2000;
07-JUN-2000;
                                                                                                                                                                                      07-JUL-2000;
11-JUL-2000;
                                                             14-AUG-2000;
                                                                                                                                                                     11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                           17-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cancer; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; reproductive system related antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human reproductive system related antigen SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAM96472;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAM96472 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15 WLYWLP 20
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5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     173 AA;
                                   2000US-0220963.
2000US-0220964.
2000US-0224518.
2000US-0224519.
2000US-0225213.
                                                                                                                                        2000US-0215135.
2000US-0216647.
2000US-0216880.
2000US-0217487.
2000US-0217496.
2000US-0218290.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2001WO-US01339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                     2000US-0190076.
2000US-0198123.
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2000US-0189874
                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-0180628
2000US-0184664
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   reproductive system disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 173;
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RESULT 4
AAM41991
ID AAM4
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                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-NOV-2000
08-NOV-2000
08-NOV-2000
08-NOV-2000
08-NOV-2000
08-NOV-2000
08-NOV-2000
17-NOV-2000
17-NOV
                   AAM41991 standard; Protein;
                                                                                                                                                                                                                                                                                                 The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be us in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-465570/50.
N-PSDB; AAL02442.
                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                    Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolated nucleic acid molecule encoding a reproductive system antigen is used in preventing, treating or ameliorating a medical condition % \left( 1\right) =\left\{ 1\right\} 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rosen
                                                                                                              114
                                                                                                              1 WLYWIP 6
|:||:|
|14 WVYWVP 11
                                                                                                                                                                                                                                                                                                                                                                                                  11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CA, Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 5130; 1297pp +
                                                                                                                                                                                                                                                                 137
                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-0246526

2000US-0246527

2000US-0246610

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                   235
                                                                                                                                                                                    Score 40; DB Pred. No. 22; Mismatches
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                   AΑ
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence Listing; English.
                                                                                                                                                                                                      DB
22;
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be used
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18-AUG-2000
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22-AUG-2000
23-AUG-2000
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23-AUG-2000
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20-SEP-2000
21-SEP-2000
22-OCT-2000
23-SEP-2000
24-SEP-2000
25-SEP-2000
26-SEP-2000
27-SEP-2000
27-SEP-2000
28-NOV-2000
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2000US-0225267
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2000US-0229349
2000US-0229349
2000US-0229349
2000US-0229513
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2000US-0229513
2000US-0231241
2000US-02313141
2000US-0231411
2000US-02341180
2000US-02341180
2000US-02341180
2000US-02344617
2000US-02346476
2000US-02346476
2000US-02346476
2000US-02346523

AAM41991;

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Best Local
                                                   Matches
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25-APR-2000;
09-JUL-2000;
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03-AUG-2000;
14-SEP-2000;
19-OCT-2000;
                                                                                                                                                               in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathies and localised neuropathies and central nervous system disease, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune System suppression, Activinyinhibin activity, chemotactic/chemokinetic activity, hammostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tang
Wang
Zhao
                                                                                                     Sequence
                                                                                                                                                                                                                                                                                              The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful
                                                                                                                                                                                                                                                                                                                                                   Example 2; SEQ ID NO 6922; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                             Novel nucleic acids and such as central nervous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-DEC-2000; 2000WO-US34263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; nootropic; immunosuppressant; cytostatic; gene therapy; cance peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200153312-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human polypeptide SEQ ID NO 6922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HYSE-) HYSEQ INC
212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             leukaemia.
                         1 WLYWIP 6
 AVMANA
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                                                                                                                                                                                                                                                                                                                                                                                                                    2001-442253/47.
DB; AAI61147.
                                                                                                                                                        disorders
                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Liu C,
Wang Z,
Zhou P,
                                                                                                                                          sequence
                                                                                                     235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000US-0488725.
2000US-0552317.
2000US-05598042.
2000US-0620312.
2000US-062031450.
2000US-0652191.
2000US-0693036.
2000US-0727344.
                                                   Conservative
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Wehrman T,
                                                                                                                                           data
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Goodrich R,
                                                               90.9%;
                                                                                                                                            for
                                                                                                                                                                                                                                                                                                                                                                             system injuries
                                                                                                                                                                                                                                                                                                                                                                                        polypeptides, useful for
                                                                                                                                          this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chen R,
, Xu C,
                                                  2
                                                              Score 40;
Pred. No.
                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drmanac
                                                                                                                                          patent did not form part of the
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                                                            DB
37;
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B AJ,
RT;
                                                                          22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Qian XB,
Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yang
                                                                         Length 235;
                                                                                                                                                                                                                                                                                                                                                                                         treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ren F, V
Zhang J;
                                                                                                                                                                                                                                                                                                                                                                                          disorders
                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wang
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CNS;
                                                Gaps
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RESULT 5

밁 Q

Similarity

Conservative

0;

Indels

0;

Gaps

0,

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AAM40205
Query Match
Best Local S
Matches 4
                                                                                                                         The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activity, Drager Syndrome system suppression, activinjoinhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JAN-2000;
25-APR-2000;
09-JUL-2000;
19-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tang
Wang
                                                         Sequence
                                                                                      specification.
                                                                                                    Note: The sequence data
                                                                                                                  C.N.S disorders
                                                                                                                                                                                                                                                                                                                                                           Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries - \ 
                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAI59361.
                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-442253/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zhao
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19-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAM40205 standard;
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Wang z
Zhou
                                                           533
                                                                                                                                                                                                                                                                                                                                 SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000US-0488725.
2000US-0552317.
2000US-0598042.
2000US-0620312.
2000US-0653450.
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2000US-0693036.
2000US-0727344.
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1 Z,
u P,
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Asundi V, Ch
Wehrman T, X
Goodrich R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immunosuppressant; cytostatic; gene therapy; cancer; s system; neuropathy; central nervous system; CNS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein;
              90.9%;
                                                                                                                                                                                                                                                                                                                              3350; 10078pp; English
                                                                                                 for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3350.
Score 40; DB Pred. No. 84; 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chen R, Ma Y,
Xu C, Xue AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drmanac RT;
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Yang Y,
                            Length 533;
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Zhang
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RESULT 6
ABG30232
В
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                                                                                                                                           Query Match
Best Local S
Matches 4
                                                                                                                                                                                                                                                                                                              polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, foremembers, come manning diagnostics, for mutations
                                                                                                                                                                       and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                  diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 20;
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23-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel human diagnostic protein #30223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-FEB-2002
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 511 WVYWVP 516
                                                                     Local Similarity
nes 4; Conserv
                                 1 WLYWIP 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      invention relates to isolated polynucleotide (I) and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID No 60591; 103pp; English.
                                                                                                                                          534
                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000US-0540217.
2000US-0649167.
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                                                                                                                                        ΑĄ,
                                                                                   90.98;
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                                                                   Pred. No. 84;
2; Mismatches
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                                                                                   DB
84;
                                                                                                    22;
                                                                   0;
                                                                                                    Length 534;
                                                                   0;
                                                                   Gaps
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RESULT 8
ABB67564
ID ABB6
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AAU32016
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PA
XX
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                                                                                                                                                                                       Matches
                                                                                                                                                                                                    Query Match
Best Local (
                                ABB67564 standard; Protein;
                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 20; Page 541; 765pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-611725/70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     stem cell proliferation; haematopoiesis; nerve tissue regeneration;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU32016;
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АВВ67564;
                                                                                                                                                                                                                                                                                        sequences of novel human secreted proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tang YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-JAN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; vaccination;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel human secreted protein #2507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immune suppression; immune stimulation; anti-inflammatory; leukaemia.
                                                                                                                   511 WVYWVP 516
                                                                                                                                                     1 WLYWIP 6
                                                                                                                                                                                    4:
                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Liu C,
                                                                                                                                                                                                                                                        534 AA;
                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-0552929
2001US-0770160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene therapy; nutritional supplement;
                                                                                                                                                                                                      90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RT
                                142
                                                                                                                                                                                    Score 40; DB Pred. No. 84; 2; Mismatches
                                                                                                                                                                                                                                                                                         of the invention
                                                                                                                                                                                      0;
                                                                                                                                                                                                                    Length 534;
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                                                                                                                                                                                      0;
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26-MAR-2002

(first entry)

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RESULT 9
AAU00427
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Best Local S
Matches 5
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                                      Key
Region
                                                                                                        Omega-3 fatty acyl desaturase; fat-1; omega-6 fatty acid; lipid; omega-3 fatty acid; omega-3 desaturase activity; food; oil; nutritional supplement; chemical feedstock.
                                                                               Caenorhabditis
                                                                                                                                                           Caenorhabditis elegans omega-3 fatty acyl desaturase fat-1 polypeptide
                                                                                                                                                                                      11-MAY-2001
                                                                                                                                                                                                                 AAU00427;
                                                                                                                                                                                                                                         AAU00427 standard; Protein; 402 AA
                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence data for this patent did not form specification, but was obtained in electronic i at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 29484; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated nucleic acid genes from Drosophila and interactions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Venter JC, Adams M,
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11-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster polypeptide SEQ ID NO 29484.
                                                                                                                                                                                                                                                                                                          53 WRYWIP
                                                                                                                                                                                                                                                                                                                                                             Local Similarity
les 5; Conserv
                                                                                                                                                                                                                                                                                                                                   1 WLYWIP 6
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DB; ABL11667.
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                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                     (first entry)
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2000US-0614150
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                                                                             elegans
                                      Location/Qualifiers 80..124
                           /note=
                                                                                                                                                                                                                                                                                                                                                                        86.4%;
            "Region containing stretches of hydrophobic residues similar to those found in other
desaturases"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , DWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        detection reagent for detecting 1000 for elucidating cell signalling and c
                                                                                                                                                                                                                                                                                                                                                            Score 38; DB Pred. No. 48; 0; Mismatches
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48;
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                                                                                                                                                                                                                                                                                                                                                                                      Length 142;
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RESULT 10
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Best Local S
Matches 4
                                                                                                                                                                                                                                                                                            22- carbon fatty acids. Recombinant expression of C. elegans fat-1 polynucleotide in a wide variety of host cells, including Arabidopsis thaliana and Saccharomyces cerevisiae, produces a polypeptide with omega-3 desaturase activity. A host cell transformed with C. elegans fat-1 polynucleotide is useful for desaturating an omega-6 fatty acid to an omega-3 fatty acid by growing the host cell under conditions under which the polypeptide is expressed. The fat-1 polypeptide is useful for producing lipids having a higher proportion of omega-3 fatty acid and the lipids are useful as food, oils, as nutritional supplements, and as
                                                                                                                                                                                                                                                                                                                                                                                                                 acyl desaturase fat-1 polypeptide. The polypeptide desaturates omega-6 fatty acid to a corresponding omega-3 fatty acid by catalysing the introduction of an omega-3 double bond into 18-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel host cell transformed with recombinant fat-1 polynucleotide encoding polypeptide which desaturates omega-6 fatty acid to corresponding omega-3 fatty acid, useful for producing lipids -
Caenorhabditis elegans fat-1 (omega-3 fatty acyl desaturase) protein.
                          26-JUL-2002
                                                     AAE22532;
                                                                              AAE22532 standard;
                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                   chemical teedstocks.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Fig 1; 17pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-FEB-2001
                                                                                                                                                 261 WYYWVP 266
                                                                                                                                                                            1 WLYWIP 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                            present sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAS00431
                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                         402 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Spychalla
                                                                                                                                                                                                      Conservative
                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97US-0038409.
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/note=
327..32
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162..163
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159
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/note= "Highly conserved in
127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      229..284
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                                                                               Protein;
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                                                                                                                                                                                                                 86.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           represents Caenorhabditis elegans omega-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Highly conserved in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Highly conserved in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             desaturases"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Highly conserved in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Highly conserved in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Highly
                                                                               402
                                                                                                                                                                                                   Score 38; DB 22;
Pred. No. 1.3e+02;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      conserved in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          stretches of hydrophobic those found in other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         membrane desaturases
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                                                                                                                                                                                                                              Length 402;
                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                       into 18-,
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Best Local
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                                                                                                                                        Human secreted protein; autoimmune disorder; hyperproliferative cardiovascular disorder; cerebrovascular disorder; angiogenesis; nervous system disorder; bacterial infection; viral infection; fungal infection; ocular disorder; wound healing; tissue regener
                                                                                                                                                                                                                                                                    AAU01575 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Recombinant expression of fat-1 gene of Caenorhabditis elegans in wide variety of cells, including cells of Arabidopsis thaliana and Saccharomyces cerevisiae, produces a polypeptide having omega-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Browse
(HUMA-) HUMAN GENOME SCI INC
                                                                                                           Homo sapiens.
                                                                                                                                                                                                  Human secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   desaturase activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-FEB-1997;
18-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US2002042933-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FAT-1 protein; omega-3 fatty acyl food oil; nutritional supplement;
                      27-SEP-1999;
                                                                                      WO200123547-A1
                                                                                                                                 epithelial cell
                                                                                                                                                                                                                        18-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Fig 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BROW/) BROWSE J A.
(SPYC/) SPYCHALLA J P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-DEC-2000;
                                           26-SEP-2000; 2000WO-US26337
                                                                                                                                                                                                                                                                                                                           261 WYYWVP 266
                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                       e present sequence is Caenorhabditis elegans FAT-1, an omega-3 fatty yl desaturase protein. FAT-1 polypeptide is useful for producing lipids ving a higher proportion of omega-3 fatty acid. Such lipids are useful food oils nutritional supplements and as chemical fedstocks.
                                                                                                                                                                                                                                                                                                                                                1 WLYWIP 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2002-361389/39.
>B; AAD35559.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JA,
                                                                                                                                                                                                                                                                                                                                                                      4;
                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                   402
                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                        (first entry)
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98US-0025578.
                     99US-0155806
                                                                                                                                                                                                  protein immunogenic
                                                                                                                                 proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20pp;
                                                                                                                                                                                                                                                                   Peptide;
                                                                                                                                                                                                                                                                                                                                                                                  86.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            English.
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Pred.
                                                                                                                                                                                                                                                                                                                                                                     ore 38; DB red. No. 1.3e Mismatches
                                                                                                                                 skin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     desaturase; chemical feedstock;
                                                                                                                                                                                                epitope encoded by
                                                                                                                                                                                                                                                                                                                                                                               DB 23;
1.3e+02;
                                                                                                                                 chemotaxis;
                                                                                                                                                                                                                                                                                                                                                                                          Length 402;
                                                                                                                                                                                                  gene
                                                                                                                                           regeneration;
                                                                                                                                                                                                                                                                                                                                                                     0;
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                                                                                                                                                                           disorder;
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RESULT 12
ABP28377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence represents a human secreted protein encoded by a nucleic CC acid of the invention. Secreted proteins and their related nucleic acids CC can be used in the diagnosis of or susceptibility to a pathological CC condition by determining the presence or absence of a mutation in a CC nucleic acid or the presence or amount of expression of a secreted protein. The sequences are used to prevent, treat or amedical CC condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, CC chickens or sheep. The antibodies to the polypeptides can also be used in CC alleviating symptoms associated with disorders and in diagnostic CC immunoassays e.g. radioimmunoassays or enzyme linkedCC immunosorbent CC arthritis, hyperproliferative disorders e.g. neoplasms of the breast or CC liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. neoplasms of the breast or CC e.g. Alzheimer's disease, infections caused by bacteria, viruses and CC e.g. Alzheimer's disease, infections caused by bacteria, viruses and ccular disorders e.g. corneal infection. The peptides can also be used to aid wound healing and epithelial cell proliferation, to help crevent skin ageing due to sunburn, to maintain organs before CC additive or preservative to alter storage capabilities.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                              27-OCT-2000;
24-NOV-2000;
07-MAR-2001;
                                                                                                                                                                                                                                    Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; antiinflammatory; infection; vaccine; meningitis; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acids encoding 26 human secreted polypeptides, useful for preventing, diagnosing and/or treating e.g. Gaucher's disease, Alzheimer's disease, Scimitar syndrome, Creutzfeldt-Jacob disease, diabetes mellitus and multiple sclerosis
                                                                                                                                                                                                                                                                                                  Streptococcus polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 387;
(CHIR-) CHIRON SPA. (GENO-) INST GENOMIC RES
                                                                                                             29-OCT-2001; 2001WO-GB04789
                                                                                                                                                                                                      Streptococcus agalactiae
                                                                                                                                                                                                                                                                                                                                  02-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                   ABP28377;
                                                                                                                                                                                                                                                                                                                                                                                                 ABP28377 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 WLYWIP 6
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                                              ; 2000GB-0026333.
; 2000GB-0028727.
; 2001GB-0005640.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ruben
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84.1%;
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                                                                                                                                                                                                                                                                                                  SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                 384
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13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (I) are used to detect Streptococcus in a biological sample. (I) is used to determine whether a compound binds t (I). A composition comprising (I) or a nucleic acid encoding (I), may used as a vaccine or diagnostic composition. The disease caused by Streptococcus that is prevented or treated may be meningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity chromotography, immunoassays, and distinguishing/identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in the specification. The proteins have antibacterial and antiinflammatory activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and antibodies that bind (I) are used in the manufacture of medicaments for the treatment of the control of the con
                           N-PSDB;
                                                                                                                                                                                            23-MAR-2000; 2000US-191637P
11-JUL-2000; 2000US-0614150
                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 3755; 4525pp; English.
                                                                                               Venter
                                                                                                                                                                                                                                                                   23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                                                                                                                                     27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                     WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB60764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABB60764 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI;
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Tettelin H;
                                                                                                                                            (PEKE
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1.9e+02;
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RESULT 14
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Best Local :
       AAU03601-AAU03722 represent Group B Streptococcus (Streptococcus agalactiae) amino acid sequences of the invention. S. agalactiae is an encapsulated bacterium which is a major pathogen of humans causing sepsis and meningitis in neonates as well as adults. The S. agalactiae antigenic polypeptides are used to vaccinate against Group B Streptococcus infections, particularly to prevent infection in new born children
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB577737-ABB72072).
                                                                                                                                                New polypeptides derived from Streptococcus agalactiae are useful to provide detection of, and vaccination against, Group B Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                              Group B Streptococcus; encapsulated bacterium; therapeutic; sepsis
meningitis; neonate; antigenic; vaccine; infection; genital tract;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated nucleic acid genes from Drosophila and
                                                                                                            Claim
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                                                                                                                                                                                                                                                                                                                      07-SEP-2000; 2000WO-GB03437
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                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus agalactiae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU03712 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 9084; 21pp + Sequence Listing;
                                                                                                                                                                                                                                                               (MICR-) MICROBIAL TECHNICS LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU03712;
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                                                                                                                                   infections, particularly to prevent infection
                                                                                                                                                                                                                                                                                                                                                  10-MAY-2001
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                                                                                                                                                                                                                                     Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          invention relates
                                                                                                                                                                                              2001-316444/33.
)B; AAS07129.
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                                                                                                         1; Fig 1; 178pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                 polysaccharide vaccination.
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5; Conserv
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                                                                                                                                                                                                                                       Wells
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
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RESULT 15
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Best Local Similarity
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Matches
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                                                                                                   The sequence was deduced from a cloe isolated from a cDNA library prepd. from peripheral T cell poly(A)+ mRNA. The gene can be used to express recombinant PTPase or derivs. useful in cancer therapy where a protein kinase is involved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Key
Region
                                                                               Sequence
                                                                                                                                                           Disclosure; Fig 1; 38pp; English.
                                                                                                                                                                                  tyrosine phosphatase.
                                                                                                                                                                                            New DNA encoding non-receptor-linked protein tyrosine phosphatase used in treating malignancies associated with protein-linked
                                                                                                                                                                                                                             WPI; 1991-295643/40.
N-PSDB; AAQ13802.
                                                                                                                                                                                                                                                                 Fischer EH,
                                                                                                                                                                                                                                                                                        (WASH-) WASHINGTON RES FOUN.
                                                                                                                                                                                                                                                                                                               14-MAR-1990;
                                                                                                                                                                                                                                                                                                                                     14-MAR-1991;
                                                                                                                                                                                                                                                                                                                                                                                  WO9113989-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    useful in the preparation of a medicament for the treatment or prophylaxis of Group B Streptococcus infection. The invention does not have the disadvantages of varied response rate associated with prior art capsid polysaccharide vaccination against Group B Streptococcus.
                                                                                                                                                                                                                                                                                                                                                           19-SEP-1991.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Active-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PTPase; malignancy; cancer.
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nes 5; Conserv
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1 WLYWIP 6
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                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                             /label= core region
377.381
/label= nuclear recognition signal
396.415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers 42..274
                                                                                                                                                                                                                                                                                                                                                                                                        /label= C-terminal
/note= "hydrophobic"
                                                                                                                                                                                                                                                                                                                                                                                                                 /label=
                                           84.1%;
83.3%;
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                                Score 37; DB 12
Pred. No. 2e+02;
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Db 382 WLYWQP 387

Search completed: January 3, 2003, 15:28:37 Job time: 28.5909 secs

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Result
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Maximum DB seq length: 2000000000
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                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Query Matc Best Local	RESULT 2 T00742 ubiquitin-binding C; Species: Homo sa C; Date: 12-Feb-199 C; Accession: T0074 R; Adams, M.D.; Lof submitted to the E A; Description: Hum A; Reference number A; Accession: T0074 A; Status: prelimin A; Molecule type: D A; Residues: 1-53 A; Cross-references C; Genetics: A; Gene: A-735G6.2 A; Map position: 133/1; A; Note: A-735G6.2	Query Matc Best Local Matches 1 WL Db 3252 WL	30 35 31 35 32 35 33 35 34 35 35 35 36 35 37 35 38 35 39 35 40 35 41 35 42 35 44 35 44 35 45 35 47 35 48 35 49 7 1997 1 171997 1
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90.9%; 66.7%;	homolog man) ence_rev y.; Zhou a.Librar mosome 1 1 anslated anc002400	95.5%; Y 83.3%; rvative	9 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
Score 40; DB 2; Length Pred. No. 39;	A-735G6.2 - human ision 12-Feb-1999 #text, , L.; Crosby, M.; Fuhrm; y, March 1998 6 BAC clone CIT9875K-A- from GB/EMBL/DDBJ ; NID:g2576344; PIDN:AAV	Score 42; DB 2; Length 39 Pred. No. 1.2e+02; 1; Mismatches 0; Indels	AF0753 B83551 T10253 B83551 B83551 F36790 S58822 T25699 S49268 A64185 A64751 D64751 D64751 A649327 ALIGNMENTS ALIGNMENTS ALIGNMENTS ALIGN
533;	_change 23-Mar-2001 ann, J.; Brandon, R.; Kir 735G6. C05812.1; PID:g2576346	3944; els 0; Gaps 0;	flagellar biosynth membrane protein M hypothetical prote membrane protein M hypothetical prote probable membrane protein M hypothetical prote probable membrane cytochrome c oxida hypothetical prote probable arginine histidine permease amino acid permeas cytochrome-c oxida cytoch

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A;Cross-references: EMBL:L06040; NID:g205212; PIDN:AAA41532.1; PID:g205213 C;Superfamily: arachidonate 5-l1poxygenase C;Keywords: oxidoreductase
                                                                                                                                                                                                                                                                   C;Accession: $30051
R;Watanabe, T.; Wedina, J.F.; Haeggstroem, J.Z.; Radmark, Eur. J. Biochem. 212, 605-612, 1993
A;Title: Molecular cloning of a 12-lipoxygenase cDNA from A;Reference number: $30051; MUID:93185682; PMID:8444196
A;Accession: $30051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ross references: GB:U04331; NID:g467216; PIDN:AAA20658.1; PID:g467217
"Experimental source: strains C57BL/6 and ICR, spleen leukocytes
A:Note: removal or substitution of Ile-663 abolished enzyme activity
R:Freire-Moar, J; Alavi-Nassab, A.; Ng, M.; Mulkins, M.; Sigal, E.
Blochim. Blophys. Acta 1254, 112-116, 1995
A:Title: Cloning and characterization of a murine macrophage lipoxygenase.
A:Reference number: 149439; MUID:95110857; PMID:7811740
A:Recession: I49439
A:Status: translated from GB/EMBL/DDBJ
A:Status: translated from GB/EMBL/DDBJ
A:Residues: 1-36, 'N', 38-118, 'Q', 120-396, 'N', 398-663 <RES>
A:Cross-references: GB:L34570; NID:g509607; PIDN:AAA64930.1; PID:g763530
C:Comment: A second arachidonate 12-lipoxygenase from mouse platelets is s
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C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C;Accession: B54075; 149439
R;Chen, X.S.; Kurre, U.; Jenkins, N.A.; Copeland, N.G.; Funk, C.D.
J. Biol. Chem. 269, 13979-13987, 1994
A;Reference number: A54075; MUID:94245713; PMID:8188678
A;Accession: B54075
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C; Superfamily: arachidonate 5-lipoxygenase
C; Keywords: oxidoreductase
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A; Residues: 1-663 <WAT>
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C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: S30051
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hypothetical protein Y53C10A.9 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000 C;Accession: T27121 R;White, S.
                                                                                                                                       R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, J. Lory, S.; Olson, M.V.; Lory, S.; Olson, M.V.; Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1564 <WIL>
A;Cross-references: EMBL:AL033536; PIDN:CAA22142.1; CESP:Y53C10A.
A;Experimental source: clone Y53C10A
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A;Title: Arachidonate 12-lipoxygenase of rat pineal glands: catalytic properties A;Reference number: I52462; MUID:94162305; PMID:8117750
A;Accession: I52462
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C;Species: Rattus sp. (rat)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 11-Jun-1999
                                                               A;Title: Complete genome A;Reference number: A8299 A;Accession: C83360
                                                                                                                                                                                                                                                             C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision
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C;Superfamily: unassigned
A; Molecule type: DNA
A; Residues: 1-211 <STO>
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A; Residues: 1-663 < RES>
                                              A;Status: preliminary
                                                                                                                                                                                                                                                                                                         hypothetical protęin PA2287 [imported] - Pseudomonas aeruginosa (strain PAO1)
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A82950; MUID:20437337; PMID:10984043
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68;
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                                                                                                                                                                                   P.; Hickey,
A.; Larbig,
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K.; L
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GB:AE004654; GB:AE004091; NID:g9948311; PIDN:AAG05675.1; GSPDB:GN

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A;Status: p.c...
A;Molecule type: DNA
A;Residues: 1-739 <WIL>
A;Cross-references: EMBL:Z68220; P!
A;Cross-references: Clone T20D3
                                    Вр
                                                              Qy
                                                                                                                                                                 A; Map position: 4
A; Introns: 205/1; 246/3; 437/2; 472/1; 643/3; 721/2
C; Superfamily: Caenorhabditis elegans hypothesical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Neurospora crassa
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change
C;Accession: T48817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Вb
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                                                                                                                                                                                                                                                                                                                           submitted to the EMBL Data Library, December 1995
A; Reference number: Z19971
A; Accession: T25030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Superfamily: Neurospora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Map position: 2
A; Introns: 56/2; 68/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-407 <SCH>
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                                                                                                                                                                                                                  A; Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein T20D3.11 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Gene: NCSP: 68B2.10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:AL353821; GSPDB:GN00112; NCSP:68B2.10
A;Experimental source: cosmid contig 68B2; strain 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; mitted to the Protein Sequence Database, April 2000 Feference number: 224541
A;Accession: T48817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein 68B2.10 [imported] - Neurospora crassa
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                                                                                                                                                                                                                                  Genetics:
                                                                                                                                                                                                                                                                                                           Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                       Species: Caenorhabditis elegans
Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
                                                                                                                                   Query Match
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loyd, C.
                                    475 WSYWIP 480
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                                                                                                                  Local
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                                                                                                   Similarity 5; Conserv
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66.7%;
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Pred. No.
                                                                                                                               Score 38;
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                                                                                                   Pred. No. 1.1d); Mismatches
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62;
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33;
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AF1079
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A;Cross-references: GB:NC_003210; PIDN:CAC98252.1; PID:g16409396; GSPDB:GN00177
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C;Accession: Arriv;
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Ausurget, O.; E
D; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; E
D; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuin, M.; Kunst, F.; Kurapkat, G.; Madueno, ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J
A;Title: Comparative genomics of Listeria species.
A;Title: Comparative genomics of Listeria species.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GDB:128098; OMIM:176887
A;Map position: 18p11.22-18p11.21
A;Introns: 120/3; 165/3; 235/3; 347/2
A;Note: list of introns may be incomplete
C;Superfamily: protein-tyrosine-phosphatase, nonreceptor type 1; protein-tyrosine-C;Keywords: alternative splicing; phosphoprotein; phosphoric monoester hydrolase;
C;Keywords: alternative splicing; phosphoprotein; phosphoric monoester hydrolase;
F;42-264/Domain: protein-tyrosine-phosphatase homology cPTP>
F;216/Active site: Cys (phosphocystaine intermediate) #status predicted
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A;Residues: 348-415 <CHA>
A;Residues: 348-415 <CHA>
R;Johnson, C.V.; Cool, D.E.; Glaccum, M.B.; Green, N.; Fischer, E.H.; Bruskin, A.;
Genomics 16, 619-629, 1993
Genomics 16, 619-629, 1993
A;Title: Isolation and mapping of human T-cell protein tyrosine phosphatase sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C:Species: Homo sapiens (man)
C:C;Date: 31-Mar-1990 #sequence_revision 02-May-1994 #text_change 07-May-1999
C;Accession: A33899; C60345; A45742
R;Cool, D.E.; Tonks, N.K.; Charbonneau, H.; Walsh, K.A.; Fischer, E.H.; Krebs, E.G.
Proc. Natl. Acad. Sci. U.S.A. 86, 5257-5261, 1989
A;Title: CDNA isolated from a human T-cell library encodes a member of the protein-ty
A; Molecule type: DNA
A; Residues: 1-461 <GLA>
                                                                                                                                                                                                                                                                                                                                                                                                              amino acid transporter homolog lmo0037 [imported] - Listeria monocytogenes (strain
C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 *sequence_revision 27-Nov-2001 *text_change 27-Nov-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 115-125; 160-170; 230-241; 413-415 < JOH>
C; Comment: This protein and protein-tyrosine-phos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Reference number: A45742; MUID:93315152; PMID:8325634
A;Accession: A45742
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
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R;Champion-Arnaud, P.; Gesnel, M.C.; Foulkes, N.; Ronsin, C.; Sassone-C Oncogene 6, 1203-1209, 1991
A;Title: Activation of transcription via AP-1 or CREB regulatory sites A;Reference number: A60345; MUID:91319401; PMID:1650442
A;Accession: C60345
                                                                A; Status: preliminary
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A; Residues: 1-415 <COO>
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Best Local
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5; Conserv
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83.3%;
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Pred. No.
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(Arg) #status predicted
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pester hydrolase; tyr
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C;Species: Drosophila melanogaster
C:Date: 23-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 29-May-1998
Ccession: S55051
A;Ccession: S55051
BMBO J. 14, 2043-2055, 1995
A;Reference number: S55051; MUID:95262644; PMID:7538070
A;Accession: S55051
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A;Introns: 118/3; 142/1; 168/3; 277/3;
C;Superfamily: SAM homology
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A;Molecule type: DNA
A;Residues: 1-938 <MAH>
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A; Introns: 19/3
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A; Experimental source:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-525 <WOO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            membrane transporter - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jan-2000
                                                                                                                      F;800-865/Domain:
                                                                                                                                                                               A;Gene: FlyBase:BicC
                                                                                                                                                                                             C; Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                           A;Cross-references: EMBL:U15928
                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ood, V.; Rajandream, M.A.; Barrell, B.G.; Murphy, 
litted to the EMBL Data Library, September 1998 
deference number: Z21954 
Accession: T41427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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2e+02;
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Biochem. Biophys. Res. Commun. 248, 879-888, 1998
A;Title: Isolation and characterization of LRP6, a novel
A;Reference number: JE0272; MUID:98369644; PMID:9704021
A;Accession: JE0273
A;Moleculo turn
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C; Superfamily: low density lipoprotein receptor-related
F; 286-323, Domain: EGF homology <EGF1>
F; 592-627, Domain: EGF homology <EGF>
F; 1207-1243/Domain: LDL receptor ligand-binding repeat F; 1249-1285/Domain: LDL receptor ligand-binding repeat F; 1288-1322/Domain: LDL receptor ligand-binding repeat F; 1326-1360/Domain: LDL receptor ligand-binding repeat P
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                                                                                                                                                                                                                                                 F;286-323/Domain: EGF homology <EGFT>
F;592-627/Domain: EGF homology <EGF>
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A; Residues: 1-1613 <B
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A; Residues: 1-1613 <BRO>
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C; Species: Homo sapiens (man)
C; Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 02-Aug-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         low density lipoprotein receptor-related protein 6 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 05-reb-1999 #sequence_revision 05-reb-1999 #text_change 02-Aug-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R.D.; Levy, E.R.; Soderman, A.R.; Metz
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repeat homology <LDL3>
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     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Arachidonate 12-lipoxygenase, leukocyte-type
ALOX12L OR ALOX15.
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MEDLINE-95110857;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                               s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EM European Bioinformatics Institute. There are no restr
                                                                                       TISSUE SPECIFICITY: FOUND IN PITUITARY AND PINEAL AS LEUKOCYTES, KIDNEY, AORTA, AND SMALL INTESTINE. SIMILARITY: BELONGS TO THE LIPOXYGENASE FAMILY.
                                                                                                  PATHWAY: Leukotrienes biosynthesis.
SUBCELLULAR LOCATION: Cytoplasmic.
TISSUE SPECIFICITY: FOUND IN PITUIT;
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16-OCT-2001 (Rel. 40, Created)
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Cathepsin S precursor (EC 3.4.22.27).
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     Dandoy-Dron F., Guillo F., Benboudjema L., Deslys J.-P., Lasmesas Dormont D., Tovey M.G., Dron M.;
Dormont D., Tovey M.G., Dron M.;
"Gene expression in scrapie. Cloning of a new scrapie-responsive and the identification of increased levels of seven other mRNA transcripts.";
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                                                              STRAIN-C57BL/6; TISSUE-Brain; MEDLINE-98184882; PubMed-9516475;
                                                                                    SEQUENCE OF 296-340 FROM N.A.
                                                                                                          Biochim.
                                                                                                                                        Soederstroem M., Salminen H., Glumoff V.,
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STRAIN-C57BL/6; TISSUE-Cartilac
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                                                                                                                                                                                                                                                                        129/Sv; TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                  Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88.6%;
66.7%;
                                                                                                         during skeletal de
1446:35-46(1999).
                                                                                                                                                                                                                                                   the EMBL/GenBank/DDBJ
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K -> N (IN REF. 2).

E -> Q (IN REF. 2).

T -> N (IN REF. 2).

T -> N (IN REF. 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                        AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NO.
                                                                                                                                                                        TISSUE SPECIFICITY
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Y SIMILARITY).
Y SIMILARITY).
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                                                                                                                   development.";
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20;
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                                                                                                                                        Kirschke H.,
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                                                                                                                                                                                                                                                    databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 662;
                                                                                                                                        Aro H.,
                                                     Lasmesas
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Matches 4
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DISULFID
                                                                                                                                                   CARBOHYD
VARIANT
                                                                                                                                                                     DISULFID DISULFID DISULFID
                                                                                                                                                                                                                                                               Hydrolase;
SIGNAL
                                                                                                                                                                                                                                                                                         Pfam; PF00112; Peptidase_C1; 1.
PRINTS; PR007705; PAPAIN.
PRODOm; PD000158; Peptidase_C1; 1.
PROSITE; PS00139; THIOL_PROTEASE_CYS; 1.
PROSITE; PS00639; THIOL_PROTEASE_HIS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
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                                                                              SEQUENCE
                                                                                                                                         CONFLICT
                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000668; Peptidase_C1.
InterPro; IPR000169; SHprot_acsite.
Pfam; PF00112; Peptidase_C1; 1.
                                                                                                                                                                                                                                                                                                                                                                 MEROPS; C01.034; -. MGD; MGI:107341; Ctss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute.
                                                                                                                                                                                                                                                    PROPEP
                                                                                                                                                                                                                                                                                  PROSITE; PS00640;
1
                                                                                                                                                                                                                                                                                                                                                                                                                                 L; AF051732; AAC05781.1; JOINED.
L; AF051727; AAC05781.1; JOINED.
3L; AF051728; AAC05781.1; JOINED.
3L; AF051726; AAC05781.1; JOINED.
BL; AF051730; AAC05781.1; JOINED.
BL; AF051730; AAC05781.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arg-|-Xaa compound.
SUBCELLULAR LOCATION: Lysosomal.
TISSUE SPECIFICITY: WIDELY EXPRESSED WITH HIGHEST EXPRESSION FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: BELONGS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CATALYTIC ACTIVITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IN NON-SKELETAL TISSUES. RELATIVELY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               activity on Z-Phe-Arg-|-NHMec,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: THIOL PROTEASE. THE BOND-SPECIFICITY OF THIS PROTEINASE IS IN PART SIMILAR TO THE SPECIFICITIES OF CATHEPSIN L AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
                 WLYWIP 6
WLFWMP
                                                                                                                                                                                                                                                                                                                                                                                     P25774;
                                                                                                                                                                                                                                                                                                                                                                                               AJ223208;
                                                                                                                                                                                                                                                                                                                                                                                                          Y18466;
                                                                                                                                                                                                                                                                                                                                                                                                                  AF038546; AAB94925.1;
AJ002386; CAA05360.1;
                                                Similarity
                                                                           34
97
106
146
340
                                      Conservative
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113
113
147
287
307
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178
1281
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                                                                                                                                                                                                                                                                        protease;
                                                                                                                                                                                                                                                                                  THIOL_PROTEASE_ASN;
                                                                                                                                                                                                  112
340
147
287
307
233
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97
106
                                                                             38438 MW;
                                               84.1%;
66.7%;
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                                      2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        is not removed.
                                                                                   MRAPGHAAIRWLFWMPLVCSVAMEÇLQRD -> MAVLDAPG VLCGNGATAER (IN REF. 2).
Y -> H (IN REF. 2).
S -> L (IN REF. 2).
S -> P (IN REF. 2).
A -> S (IN REF. 3).
                                                                                                                                                  N-LINKED (GLCNAC.
T -> M.
                                               Pred.
                                                         Score
                                                                                                                                                                                                                                CATHEPSIN S.
BY SIMILARITY.
                                                                                                                                                                                                                                                    ACTIVATION PEPTIDE (POTENTIAL).
                                                                                                                                                                                                                                                               POTENTIAL
                                                                            068E61126E2E0C0E CRC64;
                                                                                                                                                                              SIMILARITY .
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                                      Mismatches
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                                               37;
No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cathepsin
                                                                                                                                                                                                                                                                        Zymogen; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                more
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23;
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                                     0;
                                                        Length 340;
                                                                                                                                                           .) (FOTENTIAL).
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the Z-Val-Val-
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RESULT

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EMBL; M25393; AAA65997.1; --
EMBL; M81478; -; NOT_ANNOTATED_CDS.
EMBL; BC008244; AAH08244.1; --
PIR; A33899; A33899.
HSSP; P18031; 1PTY.
Genew; HGNC:9650; PTPN2.
MIM; 176887; --
                                                                                                 PRINTS; P
SMART; SM
PROSITE;
                      DOMAIN
ACT_SITE
VARSPLIC
                                                                                                                                                                                                                                                                                use by non-profit institutions as long modified and this statement is not removed: entitles requires a license agreement (See or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COOl D., Tonks N., Charbonneau H., Walsh K., Fische "cDNA isolated from a human T-cell library encodes protein-tyrosine-phosphatase family."
Proc. Natl. Acad. Sci. U.S.A. 86:5257-5261(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PTN2_HUMAN STANDARD; PRT; 4
P17706; Q96HR2;
01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HUMAN
                                                                                                                                                                                                                                                                                                                                      the
                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein-tyrosine-phosphatase.";
Proc. Natl. Acad. Sci. U.S.A. 89:499-503(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cell protein-tyrosine PTPN2 OR PTPT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUN-2002 (Rel. 41, Last annotation update) Protein-tyrosine phosphatase, non-receptor type
 SEQUENCE
                                                                       PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                          Pfam; PF00102;
                                                                                                                                                     InterPro;
                                                                                                                                                                  InterPro; IPR000387;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Eye;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORM PTPB).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mosinger B. Jr., Tillmann U., "Cloning and characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=92115688; PubMed=1731319;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=89315776; PubMed=2546150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=T-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                               Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                          SÜBCELLULAR LOCATION: Cytoplasmic.
ALTERNATIVE PRODUCTS: 2 ISOFORMS; PTPA
PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: PTPA ISOFORM IS PRO
EXPRESSED IN HUMAN TISSUES. PTPB ISOFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ween the Swiss Institute of Bioinformatics Institute. The European Bioinformatics Institute. The by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS TYROSINE PHOSPHATASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                IN PLACENTA.
                                                                                                              SM00194; PTPc; 1
                                                                                                                           o; IPR000242; Tyr_pp. F00102; Y_phosphatase; PR00700; PRTYPHPHTASE
                         42
216
382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Human)
 AA;
          Alternative splicing.
286 PROTEIN-TYROSINE PHOSPHATASE.
216 BY SIMILARITY.
415 WLYMOPILTEMMGFMSVILVGAFVGWRLFFQQNAL ->
TDT (IN ISOFORM PTPA).
 48528
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                                                                                                                                                                 TYR_phosphatase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            phosphatase) (TCPTP).
 MW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Ve
Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Westphal H., Tre of a mouse cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    update
                                                                                                                                                                                                                                                                                                                                                                                                                             IS PROBABLY
ISOFORM WAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          415
                                                                                                                                                                                                                                                                                             (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                       There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                AND PTPB (SHOWN HERE);
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                                                                                                                                                                                                                                                                                                            Usage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          encoding
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                                                                                                                                                                                                                                                                                                                                   restrictions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IP3S_HUMAN STANDARW;

[193S_HUMAN STANDARW;

Q14571; O94773;

Q1-NOV-1997 (Rel. 35, Created)

Q1-NOV-1997 (Rel. 35, Last sequence update)

15-JUN-2002 (Rel. 41, Last annotation update)

Inositol 1,45-trisphosphate receptor type 2 (Ty
                                                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Exthe European Bioinformatics Institute. There are no restructed by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (LONG ISOFORM).
MEDLINE-94363219; PubMed-8081734;
Yamamoto-Hino M., Sugiyama T., Hikiti K.,
Hasegawa K., Sekine S., Sakurada K., Miyaw
Hasegawa M., Mikoshiba K.;
"Cloning and characterization of human typ.
1,4,5-trisphosphate receptors.";
                 Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Futateugi A., Kuwajima G., Mikoshiba K.;
"Muscle-specific mRNA isoform encodes a protein composed m
N-terminal 175 residues of type 2 Ins(1,4,5)P3 receptor.";
Biochem. J. 334:559-563(1998).
                                EMBL; AB012610;
                                             EMBL; D26350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mammalia; Eutheria;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=98399819; PubMed=9729462;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Heart,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (SHORT ISOFORM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Recept. Channels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           382 WLYWQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ģ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 WLYWIP 6
                                                                                                                                                                                               DOMAIN: THE RECEPTOR CONTAINS A CALCIUM CHANNEL IN ITS C-EXTREMITY. ITS LARGE N-TERMINAL CYTOPLASMIC REGION HAS THE BINDING SITE IN THE N-TERMINUS AND MODULATORY SITES IN THE PORTION IMMEDIATELY UPSTREAM OF THE CHANNEL REGION. PTM: PHOSPHORYLATED ON TYROSINE RESIDUES (BY SIMILARITY). MISCELLANEOUS: CALCIUM APPEARS TO INHIBIT LIGAND BINDING RECEPTOR, MOST PROBABLY BY INTERACTING WITH A DISTINCT CALCIUM-BINDING PROTEIN WHICH THEN INHIBITS THE RECEPTOR. SIMILARITY: BELONGS TO THE INSP3 RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                           ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN SHORT FORM/TIPR; ARE PRODUCED BY ALTERNATIVE SPLICING TISSUE SPECIFICITY: THE SHORT ISOFORM IS FOUND IN SKE
                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: RECEPTOR FOR INOSITOL 1,4,5-TRISPHOSPHATE, A SECOND MESSENGER THAT MEDIATES THE RELEASE OF INTRACELLULAR CALCIUM. SUBUNIT: HOMOTEFRAMER (BY SIMILARITY).
SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
                                                                                                                                                                                                                                                                                                                                                 AND HEART
                HGNC:6181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                             BAA05384.1;
                                BAA33961.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2:9-22(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 37;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Eutel Catarrhini; Hominidae; Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human type 2 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Miyawaki A.,
                                                                                          (See http://www.isb-sib.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB
28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mattei M.-G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ۲,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 415;
                                                                                                                                                                                                                                                                                                                                                                                            (SHOWN HERE) AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              type 3 inositol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Furuichi T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Euteleostomi;
                                                                                                                                                                                                                                                                                                 N ITS C-TERMINAL
N HAS THE LIGAND-
ES IN THE MIDDLE
                                                                                                                                                                                                                                                                                                                                                              SKELETAL MUSCLE
                                                                                                                                        restrictions
                                                                                                           and
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isoform
                                                                                            .ch/announce/
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RESULT 6
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Best Local S
Matches 5
                   STRAIN-Sprague-Dawley;
STRAIN-Sprague-Dawley;
Magnino F., Dufour J.-F.;
Magnino F., Dufour J.-F.;
"New rat IP3R isoform 2 sequence.";
"The Function: Receptor For INOSITOL 1,4,5-TRISPHOSPHATE,
"IT FUNCTION: RECEPTOR FOR INOSITOL 1,4,5-TRISPHOSPHATE,
"The Function of the Function
                                                                                                                                                                                                                                                                                                                                                                                                                      TP3S_RAT STANDARD; PRT; 2701 AA.
P29995; Q99956;
01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Inositol 1,4,5-trisphosphate receptor type 2 (Type 2 inositol 1,4,5-trisphosphate receptor type 2 (Type 2 inositol 1,4,5-trisphosphate receptor) (Type 2 InsP3 receptor) (Type 2 InsP3R2).
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VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00520; ion_trans; 1. Pfam; PF01365; RYDR_ITPR; 2. Pfam; PF02815; MIR; 4.
                                                                                                                                                                                    "Structure of a novel InsP3 EMBO J. 10:3199-3206(1991).
                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                SEQUENCE FROM N.A
                                                                                                                                                                                                                        Mignery G.A.;
                                                                                                                                                                                                                                     Suedhof T.C.,
                                                                                                                                                                                                                                                            MEDLINE=92007769;
                                                                                                                                                                                                                                                                             TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10116
                                                                                                                                                                                                                                                                                                                                                                                                             ITPR2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 694 WLYWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 WLYWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SM00472; MIR; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PR00779;
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IPR000493; InsP3_receptor
IPR000636; M+channel_nlg.
IPR003608; MIR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transmembrane;
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                                                                                                                                                                                                                                         Newton
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                                                                                                                                                                                                                                                            PubMed=1655411;
                                                                                                                                                                                                                                                                                                                                                    Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                AND VARIANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84.18;
100.08;
                                                                                                                                                                                                                                       C.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InsP3_receptor
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Integral membrane
                                                                                                                                                                                                                                       Archer B.T.
                                                                                                                                                                                                   receptor.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 37;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PHOSPHORYLATION (POTENTIAL)
IVVGDK -> DASFWI (IN SHORT
MISSING (IN SHORT ISOFORM)).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CYTOPLASMIC (POTENTIAL).
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Sciurognathi; Muridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EB5C7DDCDD17F74A CRC64;
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                                                                                                                                                                                                                                       III,
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1.6e+02;
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                                    INTRACELLULAR CALCIUM
protein. Endoplasmic
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MGA1_YEAST

ID MCA1_YEAST STANDARD;

AC P53050;

DT 01-OCT-1996 (Rel. 34, Created)
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00520; ion_trans; 1.
Pfam; PF01365; RYDR_ITPR; 2.
Pfam; PF02815; MIR; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001682; Ca/Na_pore.
InterPro; IPR000493; Insp3_receptor.
InterPro; IPR000636; M+channel_nlg.
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                                                                                                                                                                                                                  694
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      reticulum.

DOMAIN: THE RECEPTOR CONTAINS A CALCIUM CHANNEL IN ITS C-TERMINAL DOMAIN: THE RECEPTOR CONTAINS A CALCIUM CHANNEL IN ITS C-TERMINAL CYTOPLASMIC REGION HAS THE LIGAND-EXTREMITY. ITS LARGE N-TERMINUS AND MODULATORY SITES IN THE MIDDLE PORTION IMMEDIATELY UPSTREAM OF THE CHANNEL REGION.

PTM: PHOSPHORYLATED ON TYROSINE RESIDUES (BY SIMILARITY).

SIMILARITY: BELONGS TO THE INSP3 RECEPTOR FAMILY.
                                                                                                                                                                                                                  MLYWI 698
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5; Conserv
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RESULT 8
YQ21_CAEEL
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Best Local
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Q09231;
Q1-NOV-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Analysis of a 17.9 kb region from Saccharomyces cerevisiae chromosome VII reveals the presence of eight open reading fr including BRF1 (TFILIB70) and GCN5 genes."; Yeast 13:373-37(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SGD; S0003481; MGA1.
InterPro; IPR000232; HSF_DNA_bind.
InterPro; IPR002341; HSF_ETS.
Pfam; PF00447; HSF_DNA_bind; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces. NCBI_TaxID=4932;
Caenorhabditis elegans
                  Hypothetical C09F5.1.
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00434; HSF_DOMAIN; 1. Nuclear protein; DNA-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; D29626; BAA06105.1; -.
EMBL; Y07703; CAA68970.1; -.
EMBL; Z73034; CAA97278.1; -.
HSSP; P22121; ZHTS.
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MGA1 OR YGR249W.
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                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00415; HSF;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Feroli F., Carignani G., Pavanello A., Rodrigues-Pousada C., Melchioretto P.,
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                                  protein C09F5.1 in chromosome III
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    Mismatches

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Panzeri L.,
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FLIR_SALTY
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Best Local
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                                                                                                                                                                       McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.;
                                                This
                                                                                                                                                                                                                                                                                                               MEDLINE=97464436; PubMed=9324257;
Ohnishi K., Fan F., Schoenhals G.J., Kihara M., Macnab
"The FliO, Flip, FliQ, and Flir proteins of Salmonella
putative components for flagellar assembly.";
J. Bacteriol. 179:6092-6099(1997).
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P54702;
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                                 between
                                                                                                            Nature 413:852-856(2001).
                                                                                                                                                                                                                                                   STRAIN-LT2 / SGSC1412 / ATCC 700720;
MEDLINE-21534948; PubMed-11677609;
                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A
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Bacteria; Proteobacteria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Flagellar biosynthetic
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15-JUN-2002 (Rel. 41,
15-JUN-2002 (Rel. 41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein. SEQUENCE 564 AA; 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U22832; AAA64509.1; -. WormPep; C09F5.1; CE01773.
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[1]
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                                                                                                                                                          "Complete genome sequence
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                                                                             SUBCELLULAR LOCATION: Integral membrane protein. SIMILARITY: BELONGS TO THE FLIR/MOPE/SPAR FAMILY.
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                   European
                SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
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2; Mismatches
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   as long
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 264
                                                                                                                                                         enterica
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RESULT 11
AQY1_YEAST
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RESULT 10
VG41_HSVI1
ID VG41_HSVI1
AC Q00117;
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                                                                                                                                                use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb-
                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                      Viruses; dsDNA viruses, no RN/
Ictalurid Herpes-like viruses.
NCBI_TaxID=10401;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                    SEQUENCE
                                                                                                                    EMBL; M75136; AAA88144.1;
                                                                                                                                         entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                            Virology 186:9-14(1992).
                                                                                                                                                                                                                                                  Davison A.J.;
                                                                                                                                                                                                                                                                                                                          Ictalurid herpesvirus 1 (Channel catfish virus) (CCV).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                              Hypothetical
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 HUMYWDP
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                                                                                                                                                                                                                                       catfish virus: a new type of herpesvirus.";
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66.7%;
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                                        Score 35; DB Pred. No. 43; 1; Mismatches
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7AFF46906147A63F CRC64;
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STANDARD;

PRT;

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RA Bussey H., Storms R.K., Ahmed A., Albermann K., Allen E., Ansorge W., Araujo R., Aparicio A., Barrell B.G., Badcock K., Benes V., Araujo R., Aparicio A., Barrell B.G., Badcock K., Benes V., Romann S., Bruckner M., Carpenter J., Cherry J.M., Chung E., Churcher C.M., Coster F., Davis K., Davis R.W., Chung E., Churcher C.M., Coster F., Davis K., Davis R.W., Dietrich F.S., Delius H., DiPaolo T., Dubois E., Duesterhoeft A., Duncan M., Floeth M., Fortin N., Friesen J.D., Fritz C., Goffeau A., Hunicke Smith S., Hyman R., Johnston M., Kalman S., Kleine K., Komp C., Kurdi O., Lashkari D., Lew H., Lin A., Lin D., Louis E.J., Komp C., Kurdi O., Lashkari D., Lew H., Lin A., Lin D., Louis E.J., Komp C., Kurdi O., Lashkari D., Lew H., Lin A., Lin D., Louis E.J., Messenguy F., Mewes H.-W., Mirtipati S., Moesti D., Rak Mueller-Auer S., Namath A., Nentwich U., Oefner P., Pearson D., Rak Petel F.X., Pohl T.M., Purnelle D., Schafer M., Scharfe M., Scherens B., Schramm S., Schroeder M., Solicu A.M., Tettelin H., Rak Alsh S.V., Wambutt R., Wang Y., Wedler E., Wedler H., Winnett E., The Miller A., Vo D.H., Hani J., Schroeder M., Zollner M., Zollner A., Vo D.H., Hani J., Schroeder M., Zollner M., Zollner A., Vo D.H., Hani J., Schroeder M., Zollner M., Zollner M., Zollner M., Zollner M., Vo D.H., Hani J., Schroeder M., Zollner M., Zo
    Query Match
Best Local Similarity
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                Pfam; PF00230; MIP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               between laboratory and wild-type strains.";
J. Biol. Chem. 273:27565-27572(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHARACTERIZATION.
MEDLINE=98438534; PubMed=9765289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=S288c / AB972;
MEDLINE=97313271; PubMed=9169875;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomyces cerevisiae (Baker's yeast).

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                        VARIANT
                                                                                                                                                                                                                  TRANSMEM
                                                                                                                                                                                                                                        TRANSMEM
                                                                                                                                                                                                                                                            Transport;
                                                                                                                                                                                                                                                                                  PROSITE;
                                                                                                                                                                                                                                                                                                      TIGRFAMS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bonhivers M., Carbrey J.M., Gould S.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P53386;
01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                   InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Aquaporins in Saccharomyces. Genetic and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Integral membrane protein. SIMILARITY: BELONGS TO THE MIP/AQUAPORIN FAMILY (TC 1.A.8).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: WATER-SPECIFIC CHANNEL.
                                                                                                                                                                                                                                                                                                                                                             S0006396; AQY1. rPro; IPR000425; MIP_family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LABORATORY STRAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nucleotide sequence of Saccharomyces cerevisiae chromosome XVI.";
re 387:103-105(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OR YPR192W OR P9677.5
                                                                                                                                                                                                                                                                                                                         PD000295;
                                                                                                                                                                                                                                                                                  PS00221;
                                                                                                          Transmembrane.

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P45062;
01-NOV-1995
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PROSITE; P
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                                                                                                                                                                Pfam;
                                                                                                                                                                                                       EMBL; U32793; AAC22790.1; TIGR; HI1135; -.
                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a c
between the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                         -i- FUNCTION: FIRST STEP OF THE LIPID CYCLE REACTIONS IN THE BIOSYNTHESIS OF THE CELL WALL PEPTIDOGLYCAN (BY SIMILARITY).
-i- CATALYTIC ACTIVITY: UDP-N-acetylmuramoy1-L-alany1-D-glutamy1-L-lysy1-D-alany1-D-alanine + undecapreny1 phosphate = UMP + N-acetylmuramoy1-L-alany1-D-glutamy1-L-lysy1-D-alany1-D-alanine-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Phospho-N-acetylmuramoyl-pentapeptide-transferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HAEIN
                                                                                                          PROSITE; PS013
Peptidoglycan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=Rd / KWZU / ATCC 51507;
MEDLINE=95350630; PubMed=7542800;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Haemophilus influenzae
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                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Science 269:496-512(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Venter J.C.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae
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                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Integral membrane protein (By similarity). SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 4. MRAY
                                                                                                                                                                                                                                                                                                                                                                                     PATHWAY: Peptidoglycan biosynthesis. SUBCELLULAR LOCATION: Integral membr
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PS01348; MRAY_2; 1.
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                                                                                                                                                                                         IPR000715; Glycos_transf_4.
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                                                                                                           synthesis;
                                                                                                                                                               Glycos_transi
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                                                                                POTENTIAL
                                                                                                           division;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              assembly of Haemophilus influenzae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clayton R.A., Kirkness E.F., Dougherty B.A., Merrick J.M.,
                                                                                                          Transferase;
                                                                                                                                                                                                                                                                         Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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RESULT 13
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                                                                                                                                                                                                                                                                                                                              chromosome II from Saccharomyces cerevisiae reveals 16 open reading frames, including ten new open reading frames, five previously identified genes and a homologue of the SCO1 gene.";
Yeast 10:S75-S80(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

MEDLINE-95157516; PubMed-7854312;

MEDLINE-95157516; PubMed-7854312;

Takita Y., Ohya Y., Anraku Y.;

"The CLS2 gene encodes a protein with multiple membrane-spanning domains that is important Ca2+ tolerance in yeast.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CSG2 protein precursor.
CSG2 OR CLS2 OR YBR036C OR YBR0404.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fung1; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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01-FEB-1994 (Rel. 28, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
CSG2 protein precursor.
                   the
                                                                This
                                                                                                                                                                                                       Schulze M., Roedel G.;
"Accumulation of the cytochrome c oxidase sul requires a mitochondrial membrane associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-94171742; EBeeler T.J., Gable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                         nuclear SCO1 gene.";
                                                                                                                                                                                                                                                                         MEDLINE=89281488; PubMed=2543907;
                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1-92 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 116-410 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-94378725;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "A novel protein, CSG2p,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Smits P.H.M.,
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                                                                                                 . Gen. Genet. 216:37-43(1989).
FUNCTION: REQUIRED FOR CALCIUM REGULATION. MAY RIACCUMULATION BY A NON-VACUOLE ORGANELLE.
SUBCELLULAR LOCATION: Integral membrane protein.
                      European
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                                   SWISS-PROT entry is copyright. It is produced through a collaboratic sen the Swiss Institute of Bioinformatics and the EMBL outstation in the Swiss Institute of Bioinformatics and the EMBL outstation in the Swiss Institute of Bioinformatics and the EMBL outstation in the Swiss Institute of Bioinformatics and the EMBL outstation in the Swiss Institute of Bioinformatics and the EMBL outstation in the Swiss Institute of Bioinformatics and the EMBL outstation in the Swiss Institute of Bioinformatics and the EMBL outstation in the Swiss Institute of Bioinformatics and the EMBL outstation in the Swiss Institute of Bioinformatics and the EMBL outstation in the Swiss Institute of Bioinformatics and the EMBL outstation in the Swiss Institute of Bioinformatics and the EMBL outstation in the Swiss Institute of Bioinformatics and the EMBL outstation in the Swiss Institute of Bioinformatics and the EMBL outstation in the Swiss Institute of Bioinformatics and the EMBL outstation in the Swiss Institute of Bioinformatics and the EMBL outstation in the Swiss Institute of Bioinformatics and the EMBL outstation in the Swiss Institute of Bioinformatics and the Swiss Institute of Bioinformatics and the EMBL outstation in the Swiss Institute of Bioinformatics and the Bioinformatics a
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                      Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ą,
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e K., Zhao C., Dunn
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C10D066ADCA0508D CRC64;
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                                                                                                                                                                                                           oxidase subunits I and II in
associated protein, encoded b
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Matches 4
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EMBL; L24113; AAA44533.1; -.
EMBL; Z35905; CAA84978.1; -.
EMBL; X17441; CAA35491.1; -.
EMBL; X45894; S45894.
PIR; A53392; A53392;
PIR; A53392; A53392.
SEQUENCE FROM N.A.
STRAIN=K12 / W3110;
Takemoto K., Mori H.
Yamamoto Y., Inokuch
                                                                                                                                                                                                           MMUP_ECOLI
047689;
01-NOV-1997
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                                                             Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burl Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose Mau B., Shao Y.;
                                                                                             SEQUENCE FROM N.A.

STRAIN-K12 / MG1655;

STRAIN-812 / MG1657; PubMed-9278503;

MEDLINE-97426617; PubMed-9278503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transmembrane; SIGNAL
                                                                                                                                              Bacteria; Proteobacteria; Escherichia.
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PROSITE; PS00018; EF_HAND; UNKNOWN_1.
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                                                                                                                                    NCBI_TaxID=562;
                                                                                                                                                                Escherichia
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                                            complete genome sequence nce 277:1453-1474(1997).
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001 (Rel. 40, Last annotation
S-methylmethionine permease.
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Mori H.,
Inokuchi
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66.7%;
Murayama
H., Miki
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Pred.
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EF-HAND (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL)

N-LINKED (GLCNAC. . .) (POTENTIAL)

W -> L (IN REF. 2 AND 3).

W -> L (IN REF. 2 AND 3).
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Kataoka
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58;
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, Fukuda R.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "S-methylmethionine metabolism in Escherichia coli.";
J. Bacteriol. 181:662-665(1999).
-!- FUNCTION: TRANSPORTER FOR THE INTAKE OF S-METHYLM
    Bacillus subtilis
                      Amino-acid
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i D., Lew H., Lin D., Namath A., Oefr
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RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
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RA Choi S.K., Codani J.J., Fabret C., Ferrari E., Foulger D.,
RA Choi S.K., Codani J.J., Fabret C., Ferrari E., Foulger D.,
RA Choi S.K., Codani J.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Kurita K., Lapidus A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Kurita K., Lapidus A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Medina N., Mellado R.P., Naizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Presecan E., Pujic P., Purnelle B., Rapport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadale Y.,
RA Persecan E., Pujic P., Purnelle B., Rapport G., Sadale Y.,
RA Sekiguchi A., Tacconi E., Takagai T., Takahashi H., Takamaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T.,
                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no rest
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"36kb sequence between gntZ and trnY of B. subtilis genome.";
submitted (NOY-1995) to the EMBL/GenBank/DDBJ databases.
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equires a license agreement (S email to license@isb-sib.ch).
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                    29neq0 caenorhabdi
296tz3 neurospora
001260 caenorhabdi
098gk3 rhizobium 1
046622 rattus norv
091ba4 potamotrygo
099m14 mus musculu
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014562 homo sapien
09xw49 caenorhabdi
08xzu8 ralstonia s
09v596 drosophila
09ili8 pseudomonas
021056 caenorhabdi
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45	44	43	42,	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
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Q8xtj4 ralstonia s	Q8z962 salmonella			Q35341 podospora a	Q12302 saccharomyc	listeria		Q9ktf6 vibrio chol	O42765 candida alb	Q8y9s1 listeria mo	Q9fzr2 mycoplasma		Q8x9s3 escherichia	Q9h4j9 homo sapien	Q9cjk5 pasteurella	Q8q1f7 mamestra co	Q8wn96 bos taurus		075581 homo sapien		Q965d3 dictyosteli	9	ໝ	Q9fmr7 arabidopsis		Q96xr2 sulfolobus	Q93yn4 arabidopsis	Q922e7 mus musculu

ALIGNMENTS

Z B Q	DR DR SQ	DR DR	DR.	DR DR	DR	R	RI K	RA	RX	RP R	RL	RA	RP	RN	ox.	88	36	G N	DE	DT	DT	AC AC	ID	RES Q18
Query Match 95.5%; Score 42; DB 5; Length 3944; Best Local Similarity 83.3%; Pred. No. 2.6e+02;	SMART; SM00146; PI3KC; 1. PROSITE; PS00018; EF_HAND; UNKNOWN_1. SEQUENCE 3944 AA; 452752 MW; ADI1B1971F16D923 CRC64;	PF02260; PF00454;	IPR000403;	InterPro; IPR003151; FAT. InterPro; IPR003152; FATC.	InterPro; IPR002048; EF-hand.	Science 282:2012-2018(1998).	"Genome sequence of the nematode C.elegans: A platform for investigating biology ":	•	vo	SEQUENCE FROM N.A.	Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.	Gajadsty S.;	SEQUENCE FROM N.A.		NCBI TaxID=6239;		- Caenornabolicus elegans. - Pirkarvota: Motavoa: Nomatoda: Chromadoroa: Bhahditida: Bhahditoidea:	C4/B12.1.	C47D12.1 protein.	BLrel. 19, Last	01-JAN-1998 (TrEMBLrel. 05, Last sequence update)	21	Q18667 PRELIMINARY; PRT; 3944 AA.	RESULT 1 Q18667

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RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Kadota K., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
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RA Schriml L.M., Staubil F., Suzuki R., Tomita M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Blake J., Boffelli D., Hofmann M., Hume D.A., Kaniya M., Lee N.H.,
RA Blake J., Balt C., Fletcher C., Fujita M., Gariboldi M.,
RA Blake J., Balt C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kaniya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Mordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Toyo-oka K., Wang K.H., Weltz C., Whittaker C., Wilming L.,
Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
Hayashtyaki Y., Kohida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                          Query Match
Best Local
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Submitted (JUL-2001) to the EMBL/
Submitted (JUL-2001) to the EMBL/
EMBL; RK011862; BAB27886.1; -.
EMBL; BC011313; AAH11313.1; -.
MGD; MGI:107301; D7Wsu128e.
InterPro; IPR000626; Ubiquitin.
pfam; pF00240; ubiquitin; 1.
SMART; SM00213; UBQ: 1.
014562;
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01-JAN-1998
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PROSITE;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DNA segment, Chr 7, Wayne state University 128, expressed (Unknown)
(Protein for MGC:19443).
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STRAIN-C57BL/6J; TISSUE-EMBRYO;
MEDLINE-21085660; PubMed-11217851;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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Hayashizaki Y.;
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3252 WLYWLP 3257
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                                                                                                                                                                                       WVYWVP 291
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4; Conserv
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PS50053; UBIQUITIN_2; 1.
309 AA; 33449 MW; 9063F4CB4F
                     (TrEMBLrel.
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                                                                                  PRELIMINARY;
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Pred. No. 53;
2; Mismatches
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Sciurognathi; Muridae;
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01-NOV-1999 (TrEMBLrel.
01-NOV-1999 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
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Loftus B.J., Kim U.J., Sneddon V.P., Kalush F., Brandon R., Fuhrmann J., Mason T., Crosby M.L., Barnstead M., Cronin L., Deslattes Mays A., Cao Y., Xu R.X., Kang H.L., Mitchell S., Eichler E.E., Harris P.C., Venter J.C., Adams M.D.;
"Genome duplications and other features in 12 Mb of DNA sequent of the sequence of
                                                                                                                                                                                                                                                                                                                   investigating biology.";
Science 282:2012-2018(1998).
EMBL; AL033536; CAA22142.1; -.
InterPro; IPR003439; ABC_transportr.
InterPro; IPR001623; DnaJ_N.
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Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00240; ubiquitin; 1. SMART; SM00213; UBQ; 1.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                       PRODOM; PD000006; ABC_transportr; 2.
PROSITE; PS00211; ABC_TRANSPORTER; UNKNOWN_2.
PROSITE; PS00636; DNAJ 1; UNKNOWN_1.
SEQUENCE 1564 AA; 176701 MW; DC66A3E7ED8E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (NOV-1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      White S.
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                                                                                                                                                                                                                                                                                  Pfam; PF00005; ABC_tran; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   none;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=99069613;
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   Similarity 4; Conser
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       Conservative
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Pred. No.
                                    Score 39; DB 5;
Pred. No. 3.3e+02;
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A Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
A Goorge R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
A Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
A Barandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Barandon R.C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Baseson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
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Best Local :
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                                                                                                                                                                                                                                                        MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                             STRAIN-BERKELEY;
                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Raistonia solanacearum (Pseudomonas solanacearum).
Bacteria; Proteobacteria; beta subdivision; Raistonia
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01-MAR-2002 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Genome sequence of the plant pathogen Ralstonia solanacearum."; Nature 415:497-502(2002).
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RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Zheng X.H., Zhong F.N., Zhoun X., Zhu X., Zhu X., Smith H.O.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
RT "The genome sequence of Drosophila melanogaster.";

RL Science 287:2185-2195(2000) .
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Q1-OCT-2001
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MEDLINB=20437337; PUbMed=10984043;

MEDLINB=20437337; PubMed=10984043;

Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warrener P.

Bickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou

Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.

Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.

Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;

"Complete genome sequence of Pseudomonas aeruginosa PAO1, an

opportunistic pathogen.";

Nature 406:959-964(2000).
                                                                                                                                                             EMBL; AE004654; AAG05675.1; --
Hypothetical protein; Complete
SEQUENCE 211 AA; 23043 MW;
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01-NOV-1996
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
Spychalla J.P., Browse J.;
Spychalla J.P., Browse J.;
"The fat-I gene of Caenorhabditis elegans encodes an ome acid desaturase.";
Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; L41807; AAA67369.1; ...
                             SEQUENCE
                                                            Submitted (OCT-2001) to the EMBL/GenBank/DDBJ EMBL; AL132901; CAB60955.1; -. EMBL; AL132951; CAC44309.1; -. EMBL; AL132951; CAC44309.1; -. InterPro; IPR001225; FA_desaturase.
                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE=99069613;
                                                                                                                                                                                                                                                                                                   Caenorhabditis elegans.
Eukaryota; Metazoa; Nem
                                                                                                                                                                                                                                                                                                                         01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Y67H2B.a protein (Y67H2A.8 protein).
Y67H2B.A OR Y67H2A.8.
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Q21056;
                                                   Pfam; PF00487;
                                                                                                             Sulston J.E
                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                             Science
                                                                                                                                                                                                                                                                             Rhabditidae; Peloderinae; NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                          Rhabditidae;
                                                                                                                                                                                                                                                                                                                                                                                   Q9NEQ0;
                                                                                                                                                                                                                                Submitted
                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                               investigating biology.";
Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00487; FA_desaturase; 1.
ProDom; PD001081; FA_desaturase;
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                                                                                                                                                                                    one;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Caenorhabditis elegans
                                                                                                                                                                     Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                        261 WYYWVP 266
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                                        F00487; FA_desaturase; 1. PD001081; FA_desaturase;
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                             AA;
                                                                                                                                                                                             PubMed-9851916;
                                                                                                                                                                                                                                                                                       Nematoda; Chromadorea; Rhabditida; Rhabditoidea; rinae; Caenorhabditis.
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66.7%;
      86.4%; Score 38;
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                            MW;
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Caenorhabditis.
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                            BE1B1CD794EA98C5 CRC64;
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    Length 402;
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RESULT 11
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ID Q96TZ
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O01260;
01-JUL-1997 (TrEMBLrel. 0
01-JUL-1997 (TrEMBLrel. 0
01-DEC-2001 (TrEMBLrel. 1
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01-DEC-2001 (TrEMBLrel. 19, Crea
01-DEC-2001 (TrEMBLrel. 19, Last
01-MAR-2002 (TrEMBLrel. 20, Last
Hypothetical 62.9 kDa protein.
B9B15.005.
                                                                                                                                                         T20D3.11 protein.
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                                                               Submitted (DEC-1995)
                                                                                   SEQUENCE FROM N.A.
                                                                                                                  Eukaryota; Metazoa; Nemata
Rhabditidae; Peloderinae;
                                                                                                                                       Caenorhabditis elegans.
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Pfam; PF00172; Zn_clus; 1.
PROSITE; PS00463; ZN2_CY6_FUNGAL_1;
PROSITE; PS50048; ZN2_CY6_FUNGAL_2;
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariales; Sordariaceae; Neurospora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q96TZ3
                     none;
                                                                          Lloyd C.R
                                                                                                       NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                    Transcription regulation; SEQUENCE 564 AA; 62860
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nyakatura
"Genome sequence of the nematode investigating biology.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schulte U., Aign V., Hoheisel J., Brandt P., F
Nyakatura G., Mewes H.W., Mannhaupt G.;
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ
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4; Conservative
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                                PubMed=9851916;
                                                                                                                  Nematoda; Chromadorea;
inae; Caenorhabditis.
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66.7%;
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1; Mismatches
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Pred. No.
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            C
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         .elegans:
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RESULT 13
Q6462
ID Q6462
AC Q6462
DT 01-NO
DT 01-DE
DE Prote
GN PTP-S
OS Rattu
OC Eukar
OC Mamma
OX NCB1.
RN [1]
RP SEQUE
RC STRA1
RX MEDL1
RA Reddy
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Q98GK3
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Q64622;
Q1-NOV-1996
Q1-NOV-1996
Q1-DEC-2001
                                                                                                                                        01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Protein-tyrosine-phosphatase (EC 3.1.3.48) (Fragme
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                         STRAIN=SPRAGUE-DAWLEY;
MEDLINE=96125184; PubMed=8534367;
Reddy R.S., Swarup G.;
                                                                                                   Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kaneko T., Nakamura Y., Sato S., Asamizu Watanabe A., Idesawa K., Ishikawa A., Ka Kishida Y., Kiyokawa C., Kohara M., Mats Mochizuki Y., Nakayama S., Nakazaki N., Takeuchi C., Yamada M., Tabata S.; "Complete genome structure of the nitrog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-0CT-2001 (TrEMBLrel. 18, c
01-0CT-2001 (TrEMBLrel. 20, r
01-MAR-2002 (TrEMBLrel. 20, r
01-MAR-2002 (TremBlrel. 20, r
Hypothetical protein mll3287.
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EMBL; Z68220; CAA92491.1; -.
SEQUENCE 739 AA; 85116 MW;
transmembrane protein
             Reddy R.S., Swarup G.;
"Alternative splicing
                                                                SEQUENCE FROM N.A.
                                                                             NCBI_TaxID=10116;
[1]
                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001880; MSion_channel pfam; PF00924; MS_channel; I. Hypothetical protein; Complete protein SEQUENCE 739 AA; 81423 MW; E570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Complete genome structure Mesorhizobium loti.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=381;
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5; Conserv
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generates four different for tyrosine phosphatase mRNA.";
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Pred. No. 2.46
1; Mismatches
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Sciurognathi;
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E57C8EEB5A704087 CRC64;
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., Kawashima K., Kimura
Matsumoto M., Matsuno
N., Shimpo S., Sugimot
             different forms
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                                                                                                    Vertebrata;
thi; Muridae;
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; Murinae; Rat
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Best Local S
Matches 5
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Q99M14;
01-JUN-2001 (TrEMBLrel. 17
01-JUN-2001 (TrEMBLrel. 17
r 01-MAR-2002 (TrEMBLrel. 2
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MEDITINE=20219325; PubMed=10754074;
MONO-Koyanagi K., Suga H., Katoh K., Miyata T.;
Ono-Koyanagi K., Suga H., Katoh K., Miyata T.;
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EMBL; AB033582;
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Eukaryota; Metazoa; Chordata; Cranilata; Vertebrata; Chondrichthyes;
Elasmobranchii, Squalea; Hypnosqualea; Pristiorajea; Batoidea;
Myllobatiformes; Myliobatoidei; Potamotrygonidae; Potamotrygon.
                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                Mus musculus (Mouse)
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PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
PROSITE; PS50055; TYR_PHOSPHATASE_PTP;
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InterPro; IPR000387; TYR_phosphatase.
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RA Strausberg R.;

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RL Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.

BR HSLP; BC072125; AAH02125.1; -.

DR HSSP; P25774; IBXF.

DR MEROPS; C011.034; -.

DR MEROPS; C011.034; -.

DR MEROPS; C011.034; -.

DR InterPro; IPR000668; Peptidase_C1.

DR InterPro; IPR000169; SHprot_acsite.

DR Pfam; PF00112; Peptidase_C1; 1.

DR PROUNTS; PR00705; PAPAIN.

DR PROUNTS; PR00705; PAPAIN.

DR PROSITE; PS00640; THIOL_PROTEASE_CYS; 1.

DR PROSITE; PS00640; THIOL_PROTEASE_CYS; 1.

DR PROSITE; PS00639; THIOL_PROTEASE_HIS; 1.

DR PROSITE; PS00639; THIOL_PROTEASE_HIS; 1.

RM Hydrolase; Thiol protease.

SQ SEQUENCE 340 AA; 38456 MM; 076502611F319DB7 CRC64;

SEQUENCE 340 AA; 38456 MM; 076502611F319DB7 CRC64;

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Query Match Best Local Matches	RESULT 1 US-09-025-578-2 Sequence 2, Application US/09025578 Patent No. 6194167 GENERAL INFORMATION: OMEGA-3 FAT TITLE OF INVENTION: OMEGA-3 FAT NUMBER OF SEQUENCES: 2 CORRESPONDENCE ADDRESS: 2 CORREST: One World Trade Cente STREET: One World Trade Cente STREET: 121 S.W. Salmon Stree STREET: One World Trade Cente STREET: 122 S.W. Salmon Stree STREET: One World Trade Cente STREET: One World Trade Cente STREET: United States of Ame ZIP: 97204 COMPUTER: IBM PC Compatible OPERATING SYSTEM: MS DOS SOFTWARE: WordPerfect 5.1 CURRENT APPLICATION NUMBER: US/09/025 FILING DATE: Herewith CLASSIFICATION DATA: APPLICATION DATA: APPLICATION UMBER: 60/038,40 FILING DATE: February 18, 199 CLASSIFICATION UMBER: 60/038,40 FILING DATE: FEBRUARTION: NAME: ALAN E. DOW, Ph.D. REGISTRATION UMBER: 4630 TELECOMMUNICATION INFORMATION: NAME: ALAN E. DOW, Ph.D. REFERENCE/DOCKET NUMBER: 4630 TELECOMMUNICATION INFORMATION: TELEPHONE: (503) 226-7391 TELEPHONE: GOOD 256-7891 TELEPHONE: SINGLE STRANDEDNESS: S		444444333333228 5443210987784321
simi 4;	T 1 -025-578-2 -025-578-2 -025-578-2 -026-578-2 NERAL INFORMATION: APPLICANT: John A TITLE OF INVENTION APPLICATION NUMBER OF SEQUENCES CORRESPONDENCE ADDI ADDRESSEE: One Wor: STREET: One Wor: STREET: One Wor: STREET: Oregon COUNTRY: United STATE: Oregon COUNTRY: United STATION NUMBI FILLING DATE: Hea CLASSIFICATION NUMBI FILLING DATE: Feb CLASSIFICATION NUMBI FILLEFAX: (503) TELEFAX: (503) TELEFAX: (503) TELEFAX: (503) TELEFAN: GOOR SEQUENCE CHARACTER LENGTH: 402 amii TYPE: amino acid STRANDEDNESS: si TOPOLOGY: linear		333333333333333333333333333333333333333
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Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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Patent No. 6459018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Knutzon, Debbie
TITLE OF INVENTION: POLYUNSATURATED FATTY ACIDS IN PLANTS
FILE REFERENCE: MOCO.156.00US
CURRENT APPLICATION NUMBER: US/09/330,235
CURRENT FILING DATE: 1999-06-10
PRIOR APPLICATION NUMBER: 60/089,043
PRIOR APPLICATION NUMBER: 60/089,043
PRIOR FILING DATE: 1998-06-12
NUMBER OF SEQ ID NOS: 22
                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/406,330
FILING DATE: 17-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Timian, Susan J.
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 20884/101
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 10363-1636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                            TELEFAX: (716) 263-1600 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE:
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: MIMOTOPES AND ANTI-MIMOTOPES OF TITLE OF INVENTION: HUMAN PLATELET GLYCOPROTEIN ID/IX NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Miller, Jonathan L. APPLICANT: Lyle, Vicki A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    261 WYYWVP 266
                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Rochester
                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 WLYWIP 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Nixon, Hargrave, Devans & Doyle LLP Clinton Square, P.O. Box 1051
10 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lyle, Vicki A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86.4%;
                                                                                                                                                                                                                                                                                                                        US/08/556,597
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Pred. No.
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65;
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; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-556-597-159
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US-08-190-788A-233
                                                     Matches
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                                                                                  Query Match
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CLASSIFICATION: 53U
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 07/'
APPLICATION NUMBER: US 07/'
TO DATE: 05-MAR-1992
                                                                                                                                                                                                                                         FILING DATE: 05-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Stevens, Lauren L.
REGISTRATION NUMBER: 36,691
REFERENCE/DOCKET NUMBER: 1019
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415,496-2300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
APPLICANT:
                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/190,788 FILING DATE: 02-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Peptides and Compounds That Bind to TITLE OF INVENTION: IL-1 Receptor NUMBER OF SEQUENCES: 312
CORRESPONDENCE ADDRESS:
                                                                                                                          MOLECULE TYPE:
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                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
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CITY: Palo Alto
                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE:
                                                                                                                                           TOPOLOGY:
                         1 WLYWIP 6
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WVYWQP 9
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                                                     Conservative
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                                                                                                                                                                                                                                415-424-0832
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                                                                                                                                            linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Floppy disk
                                                                                                                          peptide
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                                                                                                                                                     single
                                                                   77.3%;
66.7%;
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                                                                    Score 34;
Pred. No.
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Pred. No.
                                                     Mismatches
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                                                                   DB 1;
13;
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                                                     Indels
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                                                     Gaps
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RESULT 5 US-08-383-474B-236 ; Sequence 236, Application US/08383474B

GENERAL INFORMATION:

Barrett, Ronald

Yanofsky,

Stephen

5767234

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RESULT 6
US-08-465-391A-233
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                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Barrett
APPLICANT: Yanofsk
APPLICANT: Baldwin
                                                                                                                                                                                                                                                                               Sequence 233, Application US/08465391A Patent No. 5786331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                               3est Local Similarity 66.7
datches 4; Conservative
                                                                                         APPLICANT: Baldwin, David
APPLICANT: Jacobs, Jeff W.
APPLICANT: Bovy, Phillipe R.
APPLICANT: Leahy Ellen M.
APPLICANT: Pottorf, Richard S.
APPLICANT: INVENTION: Peptides and
TITLE OF INVENTION: IL-1 Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 415-424-0832 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
NUMBER OF SEQUENCES: 314
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
Townsend & Townsend & Crew LLP
Therefore The Contest, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
         CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/190,788
FILING DATE: 02-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: 415-496-2300
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Baldwin, David N. APPLICANT: Jacobs, Jeff W. TITLE OF INVENTION: Peptides TITLE OF INVENTION: the IL-1
                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: sir
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Stevens, Lauren L
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
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San Francisco
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linear
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66.7%;
                                                                                      Peptides and Compounds That Bind to IL-1 Receptor
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 17;
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US-08-464-538B-233
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                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 233,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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APPLICATION NUMBER: US 08,
ETILING DATE: 02-FEB-1994
CLASSIFICATION: 514
ATTORNEY_AGENT INFORMATION:
NAME: NO. 5786331V161, Veri
REGISTRATION NUMBER: 32,41
REFERENCE_DOCKET NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 01-FEB-1995
                                                                                                            STREET: I'WO CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 415-326-2400
                                                                                                                                                                                                           TITLE OF INVENTION: Peptides and TITLE OF INVENTION: IL-1 Receptor NUMBER OF SEQUENCES: 402
                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
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CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                              APPLICANT:
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           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM:
SOFTWARE: PatentI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                              COUNTRY: UZIP: 94111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                           33, Application US/08464538B
5861476
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Baldwin, David
Jacobs, Jeff W.
                                                                                                                                                                                                                                         Pottorf, Richard S.

Peptides and Compounds That Bind
                                                                                                                                                                                                                                                                                          Jacobs, Jeff W.
Bovy, Phillipe R.
                                                                                                                                                                                                                                                                                                                         Baldwin,
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66.7%;
                                                                                                                                                                                                                                                                                                                                             Stephen D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 34; DB Pred. No. 13;
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APPLICATION NUMBER: FILING DATE: 05-JUI

05-JUN-1995

US/08/464,538B

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; MOLECULE TYPE:
US-08-464-538B-233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 8
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Patent No.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION UNMBER: 30,223
REFERENCE/DOCKET NUMBER: 1652
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
                                              TELEFAX: (415) 576-03
                                                                  CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: SRyder, Joseph R.
REGISTRATION NUMBER: 39,381
REFERENCE/DOCKET NUMBER: 16528A-001850US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                         ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Barrett, Ronald W.
APPLICANT: Yanofsky, Stephen D.
TITLE OF INVENTION: Peptides and Compounds That Bind to
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid•
                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 392
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 514
PRIOR APPLICATION UDATA:
APPLICATION UDMBER: US 08/190,788
FILING DATE: 02-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 514
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/373,474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                          APPLICATION NUMBER: US/08/463,076E FILING DATE: 05-JUN-1995 CLASSIFICATION: 514 '
                                                                                                                                                                                                                                                                                                                                                                                                              CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 WVYWQP 9
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5. 5880096
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Pred. No.
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Query Match
Best Local Similarity
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US-09-372-422A-28
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                                                                                                                       US-09-372-422A-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 49
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 28
LENGTH: 257
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 28, Applica Patent No. 6313375
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Loc
Matches
                                                                                                                                                                  SEQ ID NO 26
LENGTH: 272
                                                                                                                                                                                                                                                                                                                                                                  Sequence 26, Application US/09372422A
Patent No. 6313375
                                                           Query Match
Best Local Similarity
Matches 4; Conser
                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                         APPLICANT: Rudolf Jung
APPLICANT: Francois Barrieu
APPLICANT: Francois Barrieu
TITLE OF INVENTION: Maize Aquaporins and Uses Thereof
FILE REFERENCE: 0919
CURRENT APPLICATION NUMBER: US/09/372,422A
CURRENT FILING DATE: 1999-08-11
PRIOR APPLICATION NUMBER: US 60/098,692
PRIOR FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 49
NUMBER OF SEQ ID NOS: 49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Rudolf Jung
APPLICANT: Francois Barrieu
TITLE OF INVENTION: Maize Aquaporins and Uses Thereof
FILE REFERENCE: 0919
                                                                                                                                                                                                  SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                       ORGANISM: Zea
                                                                                                                                                    TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                222 WYYWI 226
220 WVYWI 224
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                            1 WLYWI 5
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                                                            Conservative
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80.0%;
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66.7%;
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80.0%;
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Pred. No. 13;
1; Mismatches
                                                           Score 34; DB 4;
Pred. No. 1.8e+0
1; Mismatches
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Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                       1.8e+02;
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13;
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                                                                                         Length 272;
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                                                            Gaps
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                                                            0,
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; MOLECULE TYPE: US-07-745-206A-15
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US-07-745-206A-15
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US-08-991-677-4
                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Feder, Scott B
REFERENCE/DOCKET NUMBER: 5150
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-372-7842
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Chiang, Vincent L
APPLICANT: Carraway, Daniel T
APPLICANT: Smeltzer, Richard H
TITLE OF INVENTION: Production of Syringyl Lignin in Gymnosperms
FILE REFERENCE: 50617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/08991677A Patent No. 6252135
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/08/991,677A CURRENT FILING DATE: 1997-12-16 EARLIER APPLICATION NUMBER: US 60/033,381 EARLIER FILING DATE: 1996-12-16 NUMBER OF SEQ ID NOS: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Liquidambar styraciflua 08-991-677-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: APPLICANT:
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                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/07/745,206A
FILING DATE: 19910815
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Feldman, Daniel TITLE OF INVENTION: Human C: TITLE OF INVENTION: Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              224 WLKWVP 229
                                                                                                                                                                                                                                                                                                                                                                                             CITY: Chicago
STATE: Illinois
                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
                                                              LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 WLYWIP 6
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5429921
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                                                1: 823 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                             135 S. LaSalle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ellis, Steven
Williams, Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Harpold, Michael
Ellis, Steven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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            protein
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Pred. No. 3.4e+02;
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RESULT 14
US-07-745-206A-13
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                                                                                                                                                              Query Match
Best Local Similarity
~~+~hes 5; Conserve
                                                                                                                                                                                                                                   ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-311-363-15
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US-08-311-363-15
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                                      Sequence 13, Application US/07745206A Patent No. 5429921
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Best Local Similarity
Matches 5; Conser
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                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                      APPLACATE:
FILING DATE:
PRIOR APPLICATION NUMBER: US
APPLICATION NUMBER: 15-AUG-19:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                 TELEFAX: (619)238-0062
INFORMATION FOR SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICANT:
                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 823 amino acid
                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 63
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)238-0999
                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 15-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Ma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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                                                                                                                      333 WLYFIP 338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE:
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CITY: San Diego
                                                                                                                                                 1 WLYWIP 6
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Feldman, Daniel
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83.3%;
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Pred. No. 5
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Pred. No. 5.3e+02;
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Harpold, Michael Ellis, Steven

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APPLICANT: William, Daniel
APPLICANT: Weldman, Daniel
APPLICANT: McCue, Ann
APPLICANT: McCue, Ann
APPLICANT: Brenner, Robert
TITLE OF INVENTION: Human Calcium Channel Compositions and
TITLE OF INVENTION: Methods
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
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US-08-311-363-13
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Matches 5
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Patent No. 5876958
GENERAL INFORMATION:
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NAME: Feder, Scott B
REFERENCE/DOCKET NUMBER: 51:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-372-7842
INFORMATION FOR SEQ ID NO: 13:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PT POS/MS-DOS
OPERATING SYSTEM: PC POS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/311,363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 1754 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/745,206A
FILING DATE: 19910815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 1754 amino aci
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Fitch, Even, Tabin & Flannery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: McCue, Ann
APPLICANT: Feldman, Daniel
TITLE OF INVENTION: Human Calcium Channel Compositions and
TITLE OF INVENTION: Methods
                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        333 WLYFIP 338
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nes 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U.S.A. ZIP: 60603
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Ellis, Steven
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83.3%;
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Pred. No. 1.1e+03;
1; Mismatches 0;
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Search completed: January Job time : 10 secs
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                                                                                                                                                                              ; MOLECULE TYPE: protein US-08-311-363-13
                                                                                                                                  Query Match
Best Local S
                                                                                                                       Matches
                                                                                                                                                                                                                                                                            TELEFAX: (619)238-006
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                    NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-51506
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)238-0999
                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 1754 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 15-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                         333 WLYFIP 338
                                                                                                                     Local Similarity nes 5; Conserv
                                                                                       1 WLYWIP 6
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                                                                                                                       Conservative
                                                                                                                                   77.3%;
83.3%;
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Pred. No.
                                                                                                                       Mismatches
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Result
No.
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Maximum DB seq
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 Published_Applications_Aa:*

1: /cgn2_6/ptodata/1/pubpaa/U
2: /cgn2_6/ptodata/1/pubpaa/U
3: /cgn2_6/ptodata/1/pubpaa/U
4: /cgn2_6/ptodata/1/pubpaa/U
6: /cgn2_6/ptodata/1/pubpaa/U
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9: /cgn2_6/ptodata/1/pubpaa/U
10: /cgn2_6/ptodata/1/pubpaa/U
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11: /cgn2_6/ptodata/1/pubpaa/U
13: /cgn2_6/ptodata/1/pubpaa/U
14: /cgn2_6/ptodata/1/pubpaa/U
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length: 2000000000
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1 WLYWIP 6
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Maximum Match 100%
Listing first 45 summaries
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: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
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2003, 15:32:11; Search time 4.77273 Seconds (without alignments)
23.825 Million cell updates/sec
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         9 US-10-104-339-2
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110 US-09-864-761-47931
110 US-09-815-242-11186
110 US-09-815-242-11052
110 US-09-815-242-1052
110 US-09-726-643-58
110 US-09-726-643-139
110 US-09-726-643-139
110 US-09-726-643-139
110 US-09-736-626-4440
110 US-09-738-626-4440
1112 US-10-033-026-8
112 US-10-033-026-8
113 US-10-033-026-8
114 US-10-033-026-8
115 US-10-033-026-8
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        Sequence 2, Appli
Sequence 204, App
Sequence 204, App
Sequence 11186, A
Sequence 1052, Appl
Sequence 1052, Appl
Sequence 58, Appl
Sequence 58, Appl
Sequence 139, Appl
Sequence 139, Appli
Sequence 47, Appli
Sequence 47, Appli
Sequence 47, Appli
Sequence 6, Appli
Sequence 10, Appli
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RESULT 1. US-10-104-3 Sequence Patent No Patent TIT TUT TUT TUT TUT TUT TUT TUT TUT TUT	222 222 222 222 222 222 232 242 242 242	20
SQUEET TREE DAY OR DRIVE		ω
Application US/10104339 US20020170090A1 UNFORMATION: UNFORMATION: DE F INVENTION: OMEGA-3 ER OF SEQUENCES: RESPONDENCE ADDRESS: ADDRESSE: Alan E. Dow, STREET: One World Trade STATE: Oregon COUNTRY: United States ZIP: 97204 UTER READABLE FORM: MEDIUM TYPE: Disk, 3-1/ COMPUTER: IBM PC compat OPERATION SYSTEM: MS DO SOFTWARE: WORDPER: US/ FILING DATE: 21-Mar-200 CLASSIFICATION NUMBER: US/ FILING DATE: 21-Mar-200 CLASSIFICATION NUMBER: 09/ FILING DATE: CUNKNOWN R APPLICATION NUMBER: 09/ FILING DATE: AND 00: 2: FILEPHONE: (503) 226-9446 [ON FOR SEQ ID NO: 2: LENGTH: 402 amino acid STRANDEDNESS: single st TOPOLOGY: linear	777777777777777777777777777777777777777	75.0
ation US/101043 170090A1 170090A1 170090A1 170090A1 170090A1 1700 1700 1700 1700 1700 1700 1700 1	110 2255 2255 2255 2255 2255 2255 2255 2	90
/101043 /101043 Browse OMEGA- : 2 ESS: n E. Do rld Tra W. Salm 1600 1600 1600 1700 1700 1700 1700 1700	100000000000000000000000000000000000000	0
9-2 Application US/10104339 US20020170090A1 INFORMATION: LCANT: John A. Browse and James P. Spychalla LE OF INVENTION: OMEGA-3 FATTY ACID DESATURASE BER OF SEQUENCES: 2 ADDRESSE: Alan E. Dow, Ph.D. STREET: One World Trade Center 121 S. M. Salmon Street Suite 1600 CITY: Portland STATE: Oregon COUNTRY: United States of America ZIP: 97204 PUTER READABLE FORM: MEDIUM TYPE: Disk, 3-1/2 inch COMPUTER: IBM PC compatible OPERATING SYSTEM: MS DOS SOFTWARE: WORDPER: US/10/104,339 FILING DATE: 21-Mar-2002 CLASSIFICATION NUMBER: 09/747,755 FILING DATE: CHANCOWN NAME: Alan E. Dow, Ph.D. REGISTRATION NUMBER: 35,123 REFERENCE/DOCKET NUMBER: 4630-49462/AED REGISTRATION INFORMATION: TELEPHONE: (503) 226-9446 TON FOR SEQ ID NO: 2: USINCE CHARACTERISTICS: LENCTH: 402 amino acid residues TYPE: amino acid STRANDEDNESS: single stranded TOPOLOGY: linear	91 659 659 40 446 466 4665 400265 01503 11503 11503 11503 11503 11503 11503 11503 11503 11503 11503 11503	61-35
	Sequence 591, App Sequence 1659, App Sequence 15, Appl Sequence 63, Appl Sequence 1140, App Sequence 6946, App Sequence 110, App Sequence 110, App Sequence 11503, App Sequence 118, App Sequence 118, App Sequence 118, Appli Sequence 118, Appli Sequence 11897, Appli Sequence 11522, Appli Sequence 11522, Appli Sequence 11522, Appli Sequence 4894, Appli Sequence 4894, Appli Sequence 4898, App Sequence 4, Appli Sequence 29, App Sequence 29, App Sequence 4, Appli Sequence 4, Appli Sequence 902, App	equence 35892,

Secondary Metabolite Production

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Length 456, Indels

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US-09-747-755-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-747-755-2
                                    Sequence 204, Application US/09801368 Patent No. US20020128250A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                        Best Loc
Matches
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Patent No. US20020042933A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Disk, 3-1/2 inch
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICANT: Busby, Robert APPLICANT: Cali, Brian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
ATAME: Alan E. Dow, Ph.D.
REGISTRATION NUMBER: 35,123
REFERENCE/DOCKET NUMBER: 4630
TELECOMMUNICATION INFORMATION:
TELEPHONE: (503) 226,7391
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (503) 228-9446 INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: John A. Browse and James P. TITLE OF INVENTION: OMEGA-3 FATTY ACID
                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                             261 WYYWVP 266
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                                                                                                                                                                                                                                                      Local Similarity
nes 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 402 amino acid residues TYPE: amino acid STRADEDNESS: single stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Alan E. Dow, Ph.D. STREET: One World Trade Center STREET: 121 S.W. Salmon Street STREET: Sulte 1600
CITY: Portland
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ZIP: 97204
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                                                                                                                                                                                                                                                                                                                                                     linear
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66.7%;
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                                                                                                                                                                                                                                                                        Score 38;
Pred. No.
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DESATURASE
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                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 99/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 99/632,366
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR PRIOR DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: PCT/US01/00666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-864-761-47931
            PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR APPLICATION NUMBER: PCT/US01/00668
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TITLE OF INVENTION: Methods for Improving Se
FILE REFERENCE: 109272.147
CURRENT APPLICATION NUMBER: US/09/801,368
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 09/487,558
PRIOR FILING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: US 60/160,587
PRIOR FILING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 440
NUMBER OF SEQ ID NOS: 440
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Best Local Similarity
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CURRENT FILING DATE: 2001-05-23
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APPLICANT:
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APPLICANT:
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Silva, Jeff
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Salama, Sofie
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No. US20020128250Alman,
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Pred. No.
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Best Local
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NUMBER OF SEC ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEC ID NO 47931
                                                                SEQ ID NO 11186
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                                                                                                            PRIOR FILING DATE: 200 NUMBER OF SEQ ID NOS:
                                                                                                                             PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Xu, H. Howard
NITLE OF INVENTION: Identification of Essential Genes
NITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
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PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
                                                                                       SOFTWARE: FastSEQ for Windows Version 4.0
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PRIOR FILING DATE: 2001-01-29
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OTHER INFORMATION: EXPLHUMAN HIT: BF090287.1, EVALUE 3.10e-01
OTHER INFORMATION: ESPLHUMAN HIT: BF090287.1, EVALUE 3.10e-01
OTHER INFORMATION: SWISSPROT HIT: P13276, EVALUE 1.90e+00
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PRIOR APPLICATION NUMBER: PCT/US01/00662
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ORGANISM: Haemophilus influenzae
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FILING DATE: 2000-11-27
APPLICATION NUMBER: 60/257,931
FILING DATE: 2000-12-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wall, Daniel
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Zyskind, Judith W.
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Pred. No. 28;
l; Mismatches
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US-10-042-141-58
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                                                                                                                                            Sequence 58, Application US/10042141 Publication No. US20020183503A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 10052
LENGTH: 475
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CURRENT APPLICATION NUMBER: US/10/042,141
CURRENT FILING DATE: 2002-01-11
PRIOR APPLICATION NUMBER: 09/726,643
PRIOR FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: PCT/US00/15187
                                                                               APPLICANT: Ruben et al.
TITLE OF INVENTION: 26 Human secreted proteins
FILE REFERENCE: PZ040P1
FILE REFERENCE: PZ040P1
AND 141
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PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
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TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/269,308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/253,625 PRIOR FILING DATE: 2000-11-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Escherichia
                                                                                                                                                                                                                                                                     105 WLYWL 109
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Zyskind, Judith W.
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Yamamoto, Robert T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Trawick, John D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wall, Daniel
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80.0%;
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80.0%;
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Pred. No.
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Pred. No. 1
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1.3e+02;
thes 0;
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; PRIOR APPLICATION NUMBER: 60/13; PRIOR FILING DATE: 199-06-07; NUMBER OF SEQ ID NOS: 190; SOFTWARE: Patentin Ver. 2.0; SEQ ID NO 58; LENGTH: 446; TYPE: PRT; ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                     US-10-042-141-139
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US-10-042-141-58
                                                                PRIOR APPLICATION NUMBER: PCT/US00/15187
PRIOR FILING DATE: 2000-06-02
PRIOR APPLICATION NUMBER: 60/137,725
PRIOR FILING DATE: 1999-06-07
NUMBER OF SEQ ID NOS: 190
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 139
                                                                                                                                                                                                                                                                                                                                            Sequence 139, Application US/10042141 Publication No. US20020183503A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 2000-06-02
PRIOR APPLICATION NUMBER: 60/137,725
PRIOR FILING DATE: 1999-06-07
NUMBER OF SEQ ID NOS: 190
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 58
LENGTH: 446
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Best Local Similarity
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Best Local Similarity 80.0%;
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 58, Application US/09726643 Patent No. US20020028449A1
                                                                                                                                                                                                      APPLICANT: Ruben et al.
TITLE OF INVENTION: 26 Human secreted proteins
EILE REFERENCE: P.2040P1
CURRENT APPLICATION NUMBER: US/10/042,141
CURRENT FILING DATE: 2002-01-11
PRIOR APPLICATION NUMBER: 09/726,643
PRIOR FILING DATE: 2000-12-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/726,643
CURRENT FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: PCT/US00/15187
PRIOR FILING DATE: 2000-06-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Ruben et al.
TITLE OF INVENTION: 26 Human secreted proteins
FILE REFERENCE: PZ040P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-726-643-58
ORGANISM: Homo sapiews
                              LENGTH: 510
TYPE: PRT
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| 141 WVYWI 145
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Pred. No. 1.7e+02;
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          224 WLKWVP 229
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Query Match
Best Local Similarity
Whiches 4; Conserve
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                                                                                                                                                    SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 511
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Best Local Similarity
Matches 4; Conserv
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Best Local Similarity
Matches 4; Conserv
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LENGTH: 510
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                                                                                                                                                                                                                                  APPLICANT: Chiang, Vincent L
APPLICANT: Carraway, Daniel T
APPLICANT: Smeltzer, Richard H
TITLE OF INVENTION: Production of Syringyl Lignin in Gymnosperms
FILE REFERENCE: 50617/c-3532.0
CURRENT APPLICATION NUMBER: US/09/796,256A
CURRENT FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: US60/03381
PRIOR APPLICATION NUMBER: US60/03381
PRIOR FILING DATE: 1996-12-16
PRIOR FILING DATE: 1996-12-16
PRIOR APPLICATION NUMBER: 08/991677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/726,643
CURRENT FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: PCT/US00/15187
PRIOR FILING DATE: 2000-06-02
PRIOR APPLICATION NUMBER: 60/137,725
PRIOR FILING DATE: 1999-06-07
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TITLE OF INVENTION:
FILE REFERENCE: PZ
                                                                                                                                                                                                        PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE:
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                                                                                                                    ORGANISM: Liquidambar styraciflua
                                                                                                                                         TYPE: PRT
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1 WLYWIP 6
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80.0%;
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1; Mismatches
                                                  Score 34; I
Pred. No. 1
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Pred. No. 1.9e+0
                                   Mismatches
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1.9e+02;
                                                  DB 10;
1.9e+02;
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                                                                                                                                        ; TYPE: PRT ; ORGANISM: Corynebacterium glutamicum US-09-738-626-4785
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                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/738,626
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: UP 99/377484
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
INUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver: 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-738-626-4785
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                                                                   Query Match
Best Local Similarity
Matches 4; Conserv
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LENGTH: 1034
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Patent No. US20020142428A1
GENERAL INFORMATION:
APPLICANT: Hodge, Martin R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 46
LENGTH: 627
TYPE: PRT
ORGANISM: Mus musculus
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Best Local Similarity
Matches 4; Conserva
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CURRENT APPLICATION NUMBER: US/09/862,027
CURRENT FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: US 09/345,473
PRIOR FILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 82
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APPLICANT:
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 563 WLYWM 567
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                                1 WLYWI 5
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SENOH, AKIHIRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HAYASHI, MIKII
OCHIAI, KEIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANDO, SEIKO
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                                                                   Score 34; DB Pred. No. 3.5e 1; Mismatches
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Pred. No. 2.3e+02;
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3.5e+02;
                                                                                                  Length 1034;
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APPLICANI: OZAKI, AKIO
APPLICANI: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PATENTIN VET. 3.0
LENGTH: 1189
TYPE: PRT
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US-10-033-026-8
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APPLICANT: NAKAGAWA, SATOSHI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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APPLICANT: Lipscombe, Stephanle
APPLICANT: Schorge, Stephanle
TITLE OF INVENTION: HUMAN N-TYPE CALCIUM CHANNEL ISOFORM AND USES THEREOF
FILE REFERENCE: BL055/7000
CURRENT APPLICATION NUMBER: US/10/033,026
CURRENT FILING DATE: 2001-12-28
PRIOR APPLICATION NUMBER: US 09/268,163
PRIOR APPLICATION NUMBER: US 09/268,163
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: US 60/077,901
PRIOR APPLICATION NUMBER: US 66/077,901
PRIOR APPLICATION NUMBER: US 60/077,901
PRIOR FILING DATE: 1998-03-13
NUMBER OF SEQ ID NOS: 28
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333 WLYFIP 338
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SENOH, AKIHIRO
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           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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2: /cgn2_6/ptodata/1,
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                      Sequence 21, Appl
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Patent No. 53179198
Patent No. 5521296
Sequence 17, Appl
Sequence 17, Appl
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                                                                                                                                                           Sequence 15,
Sequence 407,
Sequence 40,
Sequence 1298
Sequence 3948
Sequence 18,
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CURRENT APPLICATION NUMBER: US/08/688,988B; CURRENT FILING DATE: 1996-07-31; NUMBER OF SEQ ID NOS: 48
SOFTWARE: FASTSEQ for Windows Version 3.0 EQ ID NO 40
LENGTH: 509
TYPE: PRT
ORGANISM: HOrdeum vulgare
US-08-688-988-40
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Sequence 4615 Application US/09134001C
Patent NO. 6380370
GRMERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCCOCCUS
TITLE OF INVENTION: DIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT, APPLICATION NUMBER: US/09/134,001C
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APPLICANT: LYNN DOUCETTE-Stamm et al
APPLICANT: LYNN DOUCETTE-STAMM et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 40, Applicat Patent No. 6096545 GENERAL INFORMATION:
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Lefebvre, Daniel D.
APPLICANT: Malboobi, Mohammad A.
TITLE OF INVENTION: PHOSPHATE STARVATION-INDUCIBLE PROTEINS
FILE REFERENCE: PPL96-03
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EQ ID NO 4275
LENGTH: 173
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28 LLLVIA 33
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Pred. No.
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Pred. No. 5.9e+02;
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RESULT 6
US-08-740-223A-18
; Sequence 18, Application US/08740223A
; Patent No. 6265564
; GENERAL INFORMATION:
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US-09-134-001C-4298
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APPLICANT: LYNN DOUCETTE-Stamm et al
APPLICANT: LYNN DOUCETC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
CURRENT FILING DATE: 1998-08-13
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NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 4298
LENGTH: 387
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SEQ ID NO 4615
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Best Local Similarity
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Matches 6; Conserv
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PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
                                            COUNTRY: USA
ZIP: 10591
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/055,779
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TYPE: PRT
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TITLE OF INVENTION: Expressed Ligand - Vascular
TITLE OF INVENTION: Intercellular Signalling Molecule
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
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                                                                                                                             CITY: Tarrytown
STATE: NY
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version
                                    COMPUTER:
                                                                                                                                                               ADDRESSEE: Regeneron Pharmaceuticals, STREET: 777 Old Saw Mill Road
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                   IBM Compatible SYSTEM: DOS
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Pred. No. 7.4e+02;
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CURRENT APPLICATION DATA:

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RESULT 8
US-09-202-491-4
; Sequence 4, Application US/09202491
; Patent No. 6432667
; GENERAL INFORMATION:
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Best Local Similarity
Watches 5; Conserva
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PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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FILING DATE: 25-0C1 LL.
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 60/022/999
APPLICATION NUMBER: 02-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: GTC-007 CURRENT APPLICATION NUMBER: US/09/134,001C CURRENT FILING DATE: 1998-08-13 PRIOR APPLICATION NUMBER: US 60/064/964 PRIOR FILING DATE: 1997-11-08
                                                                                                                                                                                                                                                                                       LENGTH: 503
TYPE: PRT
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LENGTH: 503 amino acid
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FRAGMENT TYPE:
                                                                                                                   268 LLLIIA 273
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LOCATION: 1...503
OTHER INFORMATION:
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REGISTRATION NUMBER: 36
REFERENCE/DOCKET NUMBER:
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Pred. No. 9.5e
1; Mismatches
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Pred. No. 9.5e+02;
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9.5e+02;
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RESULT 10
US-09-709-188-18
; Sequence 18, Application US/09709188
; Patent NO. 6441137
; GENERAL INFORMATION:
; APPLICANT: Davis et al.
; TITLE OF INVENTION: Expressed Ligand
; FILE REFERENCE: REG 333-Z
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/202,491
CURRENT FILING DATE: 1998-11-16
EARLIER APPLICATION NUMBER: PCT/US97/10728
EARLIER FILING DATE: 1997-06-19
EARLIER APPLICATION NUMBER: 60/022,999
EARLIER FILING DATE: 1996-08-02
EARLIER APPLICATION NUMBER: 60/021,087
EARLIER FILING DATE: 1996-07-02
EARLIER FILING DATE: 1996-07-02
EARLIER APPLICATION NUMBER: 60/05,926
EARLIER FILING DATE: 1996-07-02
EARLIER FILING DATE: 1996-06-19
NUMBER: OF SEO ID NOS: 14
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LENGTH: 503
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Best Local
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Patent No. 6432667
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CURRENT APPLICATION NUMBER: US/09/202,491
CURRENT FILING DATE: 1998-11-16
EARLIER APPLICATION NUMBER: POT/US97/10728
EARLIER FILING DATE: 1997-06-19
EARLIER APPLICATION NUMBER: 60/022,999
EARLIER APPLICATION NUMBER: 60/022,999
EARLIER FILING DATE: 1996-08-02
EARLIER FILING DATE: 1996-07-02
EARLIER APPLICATION NUMBER: 60/021,087
EARLIER FILING DATE: 1996-07-02
EARLIER APPLICATION NUMBER: 60/655,926
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TITLE OF INVENTION: NOVEL LIGANDS, METHODS
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ORGANISM: Homo sapiens
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12 LLLVVA 17
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Pred. No.
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Pred. No: 9
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Expressed Ligand - Vascular Intercellular Signaling Molecule $333 \cdot z$

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Query Match
Best Local Similarity
Thes 5; Conserve
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                                                                                   US-08-445-640-4
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn version 3.1 SEQ ID NO 18 LENGTH: 503
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Best Local
                                                                                                                                                                 TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                 NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: 8540
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1896
TELEFAX: 415/952-9881
                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 08/170558
FILING DATE: 20-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION UMBER: 08/157563
FILING DATE: 23-NOV-1993
ATTORNEY/AGENT INFORMATION:
ADME: 1504 T
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CURRENT FILING DATE: 2000-11-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 08/740,223
PRIOR FILING DATE: 1996-10-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 30
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APPLICANT:
                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/44
FILING DATE: 22-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 Inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Protein Tyrosine Kinases NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
                                                                                                   TOPOLOGY:
                                                                                                                                LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12 LLLVVA 17
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                                                                                             : 913 amino acids
amino acid
GY: linear
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Baron, Will F.
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Mark, Melanie R.
Scadden, David T.
                 Conservative
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                               95.8%;
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            Score 23; DB 1; Length 913; Pred. No. 1.8e+03; 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                     854C2
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Pred. No.
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Query Match
Best Local Similarity
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US-08-447-314-4
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US-08-170-558-4
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                                                                                                                   Sequence 4, Application US/08447314 Patent No. 6087144
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                                               GENERAL INFORMATION:
APPLICANT: Scadden, David T.
APPLICANT: Baker, Kevin P.
APPLICANT: Baron, Will F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4, Application US/08170558
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                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1896
TELEFAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 08/157563
FILING DATE: 23-NOV-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: PC-DOS/MS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
                               TITLE OF INVENTION: Protein Tyrosine Kinases
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 913 amino acid
CORRESPONDENCE ADDRESS
                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Protein Tyrosine Kinases NUMBER OF SEQUENCES: 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: 20-DEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER:
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STATE: California
                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
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Mark, Melanie R.
Scadden, David T.
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Baron, Will F.
                                                                                                                                                                                                                                                                                       Conservative
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20-DEC-1993
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83.3%;
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                                                                                                                                                                                                                                                                                                                     Length 913;
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COUNTRY:

USA

94080

STATE: California

1: 460 Point San Bruno Blvd South San Francisco

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Query Match
Best Local Similarity
"hes 5; Conserv?
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TELEPHONE: 415/225-1896
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                              COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb 1
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                            APPLICANT: Baker, Kevin P.
APPLICANT: Baron, Will F.
TITLE OF INVENTION: Protein Tyrosine Kinases
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 08/170558
FILING DATE: 20-DEC-1993
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/44
FILING DATE: 22-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
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MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 430 LLLIIA 435
                                                                                                                                                                                                                     ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
               APPLICATION NUMBER: US/01 FILING DATE: 22-MAY-1995
CLASSIFICATION:
                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 23-NOV-1993
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                                US/08/445,461
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                                                                                                                          360 Kb floppy disk
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Pred. No. 1.8e+03;
1; Mismatches 0;
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Query Match 95.3
Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                  TELEFAX: (212) 869-974
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
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TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 919 amino acid
                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMÁTION:
NAME: COPUZZÍ, LAURA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 76
TELECOMMUNICATION INFORMÁTION:
                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 08-NOV-19:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 913 amino acids
TYPE: amino acid
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NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,6
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE: 20-DEC-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Ullrich, Axel APPLICANT: Alves, Frauke TITLE OF INVENTION: CCK-2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 415/225-1896
                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                    MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          430 LLLIIA 435
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TELEPHONE: 415/952-9881
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U.S.A. ZIP: 10036-2711
                                                                                                  LENGTH: 919 amino acids TYPE: amino acid TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
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les 5; Conserv
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1155 Avenue of the Americas
                                                                                                                                                                                                     (212) 790-9090
(212) 869-9741/8864
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 Score 23; DB 1;
Pred. No. 1.8e+03;
1; Mismatches 0
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Pred. No. 1.8e+03;
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                                 Length 919;
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Оy Search completed: January 3, 2003, 15:34:29 Job time : 10 secs 1 LLLVIA 6 |||:|| 430 LLLIIA 435

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq
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24
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1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
                 :/cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
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0: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
0: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
1: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
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/cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2003, 15:32:11; Search time 4.77273 Seconds (without alignments)
23.825 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

19	18	17	16	15	14	13	12	11	10	9	œ	7	σ	U.	4	ω	N	ш	Result No.
23	23	23	23	23	23	23	24	24	24	24	24	24	24	24	24	24	24	24	Score
95.8					95.8		100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	Query Match I
318	292	114	100	62	47	27	859	713	713	713	713	713	504	487	478	179	179	96	Length
10	10	10	9	12	10	9	10	12	9	9	9	9	9	10	10	10	10	12	DB
US-09-815-242-10468	US-09-886-055-315	US-09-925-299-976	US-09-950-933A-40	US-10-001-870-116	US-09-864-761-34868	US-09-984-245-179	US-09-529-063-70	US-10-052-586-416	US-09-999-832A-183	US-09-978-192A-183	US-09-978-697-183	US-09-978-295A-183	US-09-738-626-4035	US-09-764-853-680	US-09-764-898-225	US-09-764-898-296	US-09-764-853-847	US-10-016-481-11	ID
1046	Sequence 315, App	Sequence 976, App	Sequence 40, Appl	Sequence 116, App	Sequence 34868, A	•	Sequence 70, Appl	Sequence 416, App	Sequence 183, App	Sequence 183, App	Sequence 183, App	Sequence 183, App	Sequence 4035, Ap	•	Sequence 225, App	Sequence 296, App	Sequence 847, App	Sequence 11, Appl	Description

4 5	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30	29	28	27	26	25	24	23	22	21	20
22	22	22	22	22	22	22	22	22	22	22	22	22	22	22	22	22	22	22	23	23	23	23	23	23	23
91.7	91.7	91.7	91.7	91.7	91.7	91.7	91.7	91.7	91.7	91.7	91.7	91.7	91.7	91.7	91.7	91.7	91.7	91.7	95.8	95.8	95.8	95.8	95.8	95.8	95.8
417	381	373	362	359	324	322	318	316	301	295	295	271	258	167	124	106	69	39	1210	913	624	513	394	377	326
10	9	10	9	10	10	10	10	10	10	9	9	9	9	12	10	9	10	10	10	10	10	9	10	9	10
US-09-815-242-10165	US-09-738-626-5049	US-09-836-602-2	US-09-712-363-184	US-09-925-302-591	US-09-912-020-245	US-09-815-242-11790	US-09-886-055-101	US-09-836-602-4	US-09-836-602-6	US-09-934-483A-5	US-09-934-483A-1	US-09-738-626-5657	US-09-965-529-25	US-10-003-152-18	US-09-893-737-262	US-09-738-626-4602	US-09-864-761-37443	US-09-864-761-47820	US-09-725-433-2	US-09-223-490-4	US-09-925-297-738	US-09-738-626-6860	US-09-925-301-1388	US-10-091-628-2	US-09-888-615-105
Sequence 10165, A	5049	Sequence 2, Appli'	Sequence 184, App	Sequence 591, App	Sequence 245, App	Sequence 11790, A		Sequence 4, Appli	Sequence 6, Appli	Sequence 5, Appli	Sequence 1, Appli	Sequence 5657, Ap	25,	Sequence 18, Appl	Sequence 262, App	Sequence 4602, Ap	Sequence 37443, A	Sequence 47820, A		Sequence 4, Appli	Sequence 738, App	Sequence 6860, Ap	Sequence 1388, Ap	Sequence 2, Appli	Sequence 105, App

ALIGNMENTS

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RESULT 2
US-09-764-853-847
Sequence 847, Application US/09764853
Patent No. US20020090672A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PJZ06
CURRENT APPLICATION UMBER: US/09/764,853
CURRENT APPLICATION and Antibodies
CURRENT APPLICATION OF THE CONSULT PALM OF THE Wrapper
Prior application data removed - consult PALM or file wrapper
                                                                                                                                                                                                                                                                                                В
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Best Local S
Matches 6
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SEQ ID NO 11
LENGTH: 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 11, Application US/10016481 Patent No. US20020115610A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Zhou, Qun-Yong
APPLICANT: Ehlert, Frederick
APPLICANT: Ehlert, Frederick
TITLE OF INVENTION: Prokineticin Polypeptides, Related
TITLE OF INVENTION: Compositions and Methods
FILE REFERENCE: P-UC 5016
CURRENT APPLICATION NUMBER: US/10/016,481
CURRENT APPLICATION NUMBER: US/10/016,481
CURRENT EILING DATE: 2001-11-01
PRIOR APPLICATION NUMBER: 60/245,882
PRIOR FILING DATE: 2000-11-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS:
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Prior application data removed - cc
NUMBER OF SEQ ID NOS: 311
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 296
LENGTH: 179
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; NAME/KEY: SITE

; LOCATION: (178)

; OTHER INFORMATION: Xaa

US-09-764-853-847
                                                                                          US-09-764-898-225
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Sequence 225, Application US/09764898 Patent NO. US20020090673A1
GENERAL INFORMATION:
APPLICANT: ROSEN et al.
TITLE OF INVENTION: Nucleic Acids, P.
FILE REFERENCE: PJZ01,
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 847
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NAME/KEY: SITE
LOCATION: (6)
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NAME/KEY: SITE
LOCATION: (6)
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                                                                                                                                                                                                                                                                                                      NAME/KEY: SITE
LOCATION: (178)
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                     Antibodies
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; Prior application data removed - co
; NUMBER OF SEQ ID NOS: 311
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 225
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-898-225
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Best Local S
Matches 6
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SEQ ID NO 680
LENGTH: 487
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                Sequence 4035, Application US/09738626 Publication No. US20020197605A1 GENERAL INFORMATION:
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                                                                                                                 APPLICANT:
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PJZ06
CURRENT APPLICATION NUMBER: US/09/764,853
CURRENT FILING DATE: 2001-01-17
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
                                                            APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
                                                                                                                                                                                                                                 APPLICANT: NAKAGAWA, SATOSHI APPLICANT: MIZOGUCHI, HIROS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Prior application data removed - NUMBER OF SEQ ID NOS: 939
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NAME/KEY: SITE
LOCATION: (6)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
IKEDA, MASATO
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ANDO, SEIKO
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RESULT 7
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TYPE: PRT
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Best Local
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APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C11
FILE REFERENCE: P2630P1C11
FILE REFERENCE: P2630P1C11
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PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/978,295A CURRENT FILING DATE: 2001-10-15
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PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
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APPLICATION NUMBER: 60/065311
FILING DATE: 1997-11-13
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APPLICATION NUMBER: 60/077641
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Shelton, David L.
Stewart, Timothy A.
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Kljavin, Ivar J.
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Grimaldi, J. Christopher
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DR APPLICATION NUMBER: 60/081049
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OR APPLICATION NUMBER: 60/081195
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APPLICATION NUMBER: 60/079689
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PRIOR PPLICATION NUMBER: 60/062250
PRIOR PRILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
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PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/066364
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Shelton, David L.
Stewart, Timothy A.
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Hillan, Kenneth
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Wei-Qiang
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OR APPLICATION NUMBER: 60/084640

OR FILING DATE: 1998-05-07

OR APPLICATION NUMBER: 60/084598

OR FILING DATE: 1998-05-07

OR APPLICATION NUMBER: 60/084600

OR FILING DATE: 1998-5-07

OR APPLICATION NUMBER: 60/084627

OR APPLICATION NUMBER: 60/084643

OR FILING DATE: 1998-05-07

OR APPLICATION NUMBER: 60/085339

OR FILING DATE: 1998-05-13

OR APPLICATION NUMBER: 60/085339

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OR APPLICATION NUMBER: 60/083742
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OR FILING DATE: 1998-05-05
OR APPLICATION NUMBER: 60/084414
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OR APPLICATION NUMBER: 60/083496
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R APPLICATION NUMBER: 60/083322

DR FILING DATE: 1998-04-28

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DR APPLICATION NUMBER: 60/083495
R FILING DATE: 1998-05-15
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PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/06577
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APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and
TITLE OF INVENTION: Acids Encoding the Same
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APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
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FILING DATE: 1997-11-13
APPLICATION NUMBER: 60/066364
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   FILING DATE: 1998-03-20
APPLICATION NUMBER: 60/078910
FILING DATE: 1998-03-20
APPLICATION NUMBER: 60/078939
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                                                                                             APPLICATION NUMBER: 60/078886 FILING DATE: 1998-03-20
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Grimaldi, J. Christopher
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Hillan, Kenneth J
Kljavin, Ivar J.
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Filvaroff,
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ff, Ellen
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PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080333
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PRIOR APPLICATION NUMBER: 60/081049
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PRIOR APPLICATION NUMBER: 60/080327
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OR APPLICATION NUMBER: 60/082700
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APPLICATION NUMBER: 60/081952
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CURRENT FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: 09/91858
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides
TITLE OF INVENTION: Acids Encoding the Same
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RAPPLICATION NUMBER: 60/077632

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OR APPLICATION NUMBER: 60/077641

OR FILING DATE: 1998-03-11

OR APPLICATION NUMBER: 60/077649

OR FILING DATE: 1998-03-11

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Botstein, David
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Shelton, David L.
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Grimaldi, J. C
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RESULT 11
US-10-052-586-416
Sequence 416, Application US/10052586
Patent No. US20020127584A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian

NUMBER: 1998-04-01 1998-03-31

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PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063120
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OR APPLICATION NUMBER: 60/068017
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FILING DATE: 1997-11-24
APPLICATION NUMBER: 60/066772
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APPLICATION NUMBER: 60/065311
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FILING DATE: 1997-09-18
APPLICATION NUMBER: 60/059266
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APPLICATION NUMBER: 60/080107
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Godowski, Paul J
Gurney, Austin L
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Watanabe, Colin
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OR APPLICATION NUMBER: 60/082568

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OR APPLICATION NUMBER: 60/082569

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OR APPLICATION NUMBER: 60/082704

OR APPLICATION NUMBER: 60/082704

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R APPLICATION NUMBER: 60/084366

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OR APPLICATION NUMBER: 60/084414

R FILING DATE: 1998-05-06

R APPLICATION NUMBER: 60/084639

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R FILING DATE: 1998-06-02
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APPLICATION NUMBER: 60/083559
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Patent No. US20020102542A1
GENERAL INFORMATION:
           APPLICANT: FUKUSHIMA, DAIKICHI
APPLICANT: SHIBAYAMA, SHIRO
APPLICANT: TADA, HIDEAKI
TITLE OF INVENTION: POLYPEPTIDE, CDNA ENCODING
TITLE OF INVENTION: THE BOTH
FILE REFERENCE: Q58769
CURRENT APPLICATION NUMBER: US/09/529,063
CURRENT FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: PCT/JP98/04514
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LENGTH: 859
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PRIOR APPLICATION NUMBER: US 60/048,188
PRIOR APPLICATION 1997-05-30
PRIOR PRIOR DATE: 1997-05-30
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PRIOR APPLICATION NUMBER: JP 7
PRIOR FILING DATE: 1997-10-07
NUMBER OF SEQ ID NOS: 117
SOFTMARE: Patentin Ver. 2.1
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PRIOR APPLICATION NUMBER: US 60/041,276
PRIOR FILING DATE: 1997-03-21
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PRIOR APPLICATION NUMBER: US 60/042,344
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PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: US 60/041,277
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CURRENT FILING DATE: 2001-10-29
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             R FILING DATE: 1997-05-30
A APPLICATION NUMBER: US 60/048,355
R FILING DATE: 1997-05-30
A PPLICATION NUMBER: US 60/048,160
R FILING DATE: 1997-05-30
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; ORGANISM: Homo sapiens 
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-x-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 1997-US-30
PRIOR APPLICATION NUMBER: US 60/048,154
                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 09/632,366 PRIOR FILING DATE: 2000-08-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 2000-02-04 PRIOR APPLICATION NUMBER: US 60/207,456
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PRIOR APPLICATION NUMBER: US 60/054,804
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/180,312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 2000-05-26
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                                                                                                                                                                      FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00663
FILING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: PCT/US01/00667
                                                             APPLICATION NUMBER: PCT/US01/00670
                                                                               APPLICATION NUMBER: PCT/US01/00661 FILING DATE: 2001-01-30
                                                                                                                             FILING DATE:
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APPLICATION NUMBER: US 60/234,687 FILING DATE: 2000-09-21
                                        FILING DATE:
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Hanzel, David K.
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Pred. No.
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OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 3.8
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 3.8
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.7
OTHER INFORMATION: EXPRESSED IN LOUER AND SIGNAL = 10
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.8
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.5
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 4.2
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 4.2
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.9
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.8
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.8
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.3
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.5
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.6
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                                                                                                                                    Matches
                                                                                                                                                                Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Salceda, Susana
APPLICANT: Macina, Roberto
APPLICANT: Recipon, Herve
APPLICANT: Sun, Yongming
APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Compositions and Methods Relating to Prostate Specific Genes
FILE REFERENCE: DEST-0283
CURRENT APPLICATION NUMBER: US/10/001,870
CURRENT FILING DATE: 2001-11-20
CURRENT FILING DATE: 2001-11-20
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PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engin
                                                                                                                                                                                                                                                                                                                                 LENGTH: 62
TYPE: PRT
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TYPE: PRT
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29 LLLVVA 34
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Pred. No.
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SUMMARIES
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22	22	21	20	22	22	23	23	23	23	22	21	21	20	22	23	20	21	23	22	23	22	21	22	23	22	23	22	21	22	22	21	21	21	21
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Human novel protei	Human EST encoded	_	Polypeptide identi	Human PRO14 protei	Novel human diagno	Human G protein-co	Human PRO724 prote	Human polypeptide	Human angiogenesis	0	TANGO 1	Human PRO724 (UNQ3	Human PRO724 prote	Human polypeptide,		пď	Murine TANGO 136 p	9	C glutamicum prote	Human zcytor19 pro		t and o	Human novel secret	s pol	Escherichia coli p	Herbicidally activ	idermi	ORFX (Novel human diagno	t			is thali	Arabidopsis thalia

ALIGNMENTS

RESULT 1 AAU11836 ID AAU1

AAU11836 standard; peptide; 6 AA.

AAU11836;

Prion protein; Prp; ligand; octapeptide motif; scrapie; prion-associated disease; Creutzfeldt-Jakob disease; Gerstmann-Straussler-Scheinker disease; fatal familial insomnia; feline spongiform encephalopathy; bovine spongiform encephalopathy; transmissible mink encephalopathy; exotic ungulate encephalopathy; chronic wasting disease. WPI; 2002-061944/08 Hammond DJ, 05-APR-2001; 2001WO-US11150 (VITE-) VI 05-APR-2000; 2000US-0543188 18-OCT-2001. WO200177687-A2 Synthetic. Peptide ligand for Prion protein, 26-MAR-2002 TECHNOLOGIES INC Wiltshire VR, (first entry) Carbonell R, PrP, #11. Shen

Result No.

Score

Query Match Length

DВ

ID

Description

for

10987654321

2244444

100.0 100.0 100.0 100.0 100.0 100.0 100.0

67 67 93 140 173 179 179 179

AAU11836 AAB34100 AAG6189 ABP05389 ABB90320 ABB939430 ABB939430 ABB10539 AAU18139 AAU18690 AAU17055

Novel

Renal

novel secret and cardiova human uterin

Human polypeptide Staphylococcus epi Human cDNA SEQ ID

Human ORFX protein Human secreted pro Arabidopsis thalia Peptide ligand

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
 New isolated nucleic acid molecules encoding 49 human secreted proteins used for preventing, treating or ameliorating medical conditions, for diagnosing pathological conditions or as food additives or preservatives
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a ligand of less than 6 kD that binds to a polypeptide containing the sequence GlyTyrGlyGlyProHisGlyGly (A) or an analogue that is the retro-inverso isomer of (A). The sequence A is an octapeptide motif from the prion protein (PrP). The ligands are identified by binding assays with the peptide (A) or peptides containing (A). The ligands are used for detecting prion proteins (or prions) in biological or environmental samples, e.g. for diagnosis, also for removing them from samples, for treating or retarding development of prion-associated diseases, sepecially Creutzfeldt-Jakob diseases (in latrogenic, new variant, familial or sporadic forms), but also Gerstmann-Straussler-Scheinker disease, familial insomnia,
                                                                                                                                                                                                               19-MAR-1999;
10-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                           antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; ophthalmological; vulnerary; gene therapy; autoimmune disease; hyperproliferative disorder; neoplasm; cancer; cardiovascular disorder; cerebrovascular disorder; angiogenesis; nervous system disorder; infection; ocular disorder; wound healing; skin aging; food additive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              scrapie, bovine or feline spongiform encephalopathy, transmissible or exotic ungulate encephalopathy, or chronic wasting disease. The present sequence is a ligand of the invention.
                                                                                                                                             Rosen CA,
                                                                                                                                                                                                                                                                                                                               WO200056755-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB34100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB34100 standard;
                                                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                 16-MAR-2000; 2000WO-US06830.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                 28-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    octapeptide motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New ligands for prion proteins, useful for detection or removal or prions and for treating prion-associated diseases, recognize a specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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                                                                                                                                                                                                                                                                                                                                                               sapiens
                                                                                                              2000-587661/55.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               secreted protein; diagnosis; antiarthritic; immunosuppressive;
                                                                                              AAC59457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Page 34; 47pp;
                                                                                                                                               Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q
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ilarity 100.0%;
Conservative 0
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                                                                                                                                                                                                             99US-0125361
99US-0169910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein sequence encoded by gene 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein;
                                                                                                                                               Komatsoulis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   English
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Pred. No. 7.8e+05;
Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and vulnerary. The polynucleotides and polypeptides can be used to rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a nutoimmune diseases, hyperproliferative disorders e.g. neoplasms or cancer of the breast or liver, cardiovascular disorders, infections caused by bacteria, viruses and fungi and ocular disorders. The polypeptides can consistent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can as a food additive or preservative to increase or decrease storage capabilities. AAC59440 to AAC59448 and AAB34091 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Loc
Matches
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08-APR-1999;
16-APR-1999;
19-APR-1999;
                                           09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
25-MAR-1999;
29-MAR-1999;
01-APR-1999;
06-APR-1999;
                                                                                                                                               25-FEB-1999;
05-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and cells the genes are expressed in. Examples of activities include: antiarthritic; immunosuppressive; antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; noctropic; neuroprotective; antibacterial; virucide; fungicide; ophthalmological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human secreted proteins given in human sequences and proteins AAB34216 represent human secreted polypeptide sequences and proteins homologous to them, which are given in the exemplification of the present homologous to them, which are given in the exemplification of the tissue invention. Human secreted proteins have activities based on the tissue invention.
                                                                                                                                                                                                                                                              EP1033405-A2
                                                                                                                                                                                                                                                                                                                                                           Protein identification; signal transduction pathway; metabolic
                                                                                                                                                                                                                                                                                                                                                                                                                             18-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 11; Page 366; 419pp; English.
                                                                                                                                                                                                25-FEB-2000;
                                                                                                                                                                                                                                                                                             Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                       hybridisation assay; genetic mapping; gene expression control;
                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana protein fragment SEQ ID NO: 80003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAG61661 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 LLLVIA
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                                                                                                                                                                                                                                                                                                                             sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                2000EP-0301439
           99US-0126264.
99US-0126785.
99US-0127462.
99US-0128234.
99US-0128714.
99US-0129845.
                                                                                                               99US-0125788
                                                                                                                              99US-0123180
99US-0123548
                                                                                                                                                              99US-0121825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67
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Pred. No. 1.3e+02;
; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                            promoter;
                                                                                                                                                                                                                                                                                                                                                          pathway;
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6 - MAY 199 7 - MAY 199 9 - MAY 199 1 - JUN 199 0 - JUN 199 0 - JUN 199 8 - JUN 199 8 - JUN 199 8 - JUN 199 8 - JUN 199 9 - JU	19
99US-0132486 99US-0132863 99US-0132863 99US-0134218 99US-0134218 99US-0134219 99US-0134370 99US-0135124 99US-0135124 99US-01356021 99US-0136021 99US-0136782 99US-0137528 99US-0137528 99US-0137528 99US-0139456 99US-0139456 99US-0139456 99US-0139453 99US-0140823 99US-0140823 99US-0142920 99US-0142920 99US-0142920 99US-0142920 99US-0142920 99US-0144085 99US-0144334 99US-0144331 99US-0144333	s-0113 s-0113 s-0113
PR 22-JUL-1999; PR 23-JUL-1999; PR 23-JUL-1999; PR 23-JUL-1999; PR 26-JUL-1999; PR 26-JUL-1999; PR 27-JUL-1999; PR 28-JUL-1999; PR 28-JUL-1999	20-JUL-199 20-JUL-199 20-JUL-199 21-JUL-199 21-JUL-199 21-JUL-199 22-JUL-199
99US-0145188 99US-0145185 99US-0145185 99US-0145218 99US-0145218 99US-0145218 99US-0145218 99US-0145918 99US-0145918 99US-0145919 99US-0146386 99US-0146388 99US-0146388 99US-0147102 99US-0147103 99US-0147103 99US-0147103 99US-0147103 99US-0147103 99US-0147103 99US-0147103 99US-0147103 99US-0147103 99US-0151066 99US-0151066 99US-0151066 99US-0151066 99US-0151066 99US-0151066 99US-0151066 99US-0151066 99US-0155183 99US-015548684 99US-01554869 99US-01558369 99US-01558369 99US-01558369 99US-01558369 99US-01558369 99US-01558369	9US-014435 9US-014463 9US-014488 9US-014508 9US-014508 9US-014508

14-OCT-1999; 14-OCT-1999; 14-OCT-1999;

99US-0159637 99US-0159638 99US-0159331

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Best Local :
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22-OCT-1999
22-OCT-1999
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25-OCT-1999
25-OCT-1999
 Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders .
                                                                                                                      30-MAY-2000;
29-AUG-2000;
                                                                                                                                                                                                                                    myasthenia gravis
                                                                                                                                                                                                                                            autoimmune disorder; rheumatoid arthritis; autoimmune
                                                                                                                                                                                                                                                                         hyperproliferative disorder; psoriasis; benign tumour; haemorrhage; degenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systemic lupus erythematosus;
                                                                                                                                                    29-MAY-2001;
                                                                                                                                                                         06-DEC-2001.
                                                                                                                                                                                             WO200192523-A2
                                                                                                                                                                                                                                                                                                         Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis;
                                                                                                                                                                                                                                                                                                                               Human ORFX protein sequence SEQ ID NO:10760.
                                                                                                                                                                                                                                                                                                                                                    25-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                         ABP05389;
                                                                                                 (CURA-) CURAGEN CORP
                                                                                                                                                                                                                  Homo
                                                                                                                                                                                                                                                                 hypertension; hypothyroidism; cholesterol ester storage disease;
                                                                                                                                                                                                                                                                                                                                                                                            ABP05389 standard;
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1-OCT-1999;
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                                                          2002-106308/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                              LLLVIA 17
                                                                                                                                                                                                                                                         deficiency;
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                                                ABN21141.
                                                                             RΑ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                      2000US-206132P
2000US-228716P
                                                                                                                                                    2001WO-US10836
                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                             Leach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0160980
99US-0160981
99US-0161404
99US-0161404
99US-0161405
99US-0161360
99US-0161359
99US-0161361
99US-0161361
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99US-0161993
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99US-0160815
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                                                                                                                                                                                                                                                          immune disorder;
                                                                                                                                                                                                                                                                                                                                                                                            Protein; 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 24; DB 21;
Pred. No. 2.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                       infectious disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                              thyroiditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0,
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В

19 LLLVIA

24

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Best Local S
Matches 6
                                                                                                                                                                                                                                                                                                                                                            diseases, autoimmune disorders such as multiple sclerosis, rheumatoid arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. ORFX proteins are also
                                                                                                                                                                                         N.B. The sequence data for this patent did not form specification, but was obtained in electronic format at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                           bone degenerative disorders, or periodontal disease, and for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues and conditions resulting from
                                                                                                                                                                                                                                                                                                                                                                                                                           transplantation, cardiovascular diseases, diabetes mellitus, systemic lupus erythematosus, hypertension, hypothyroidism, cholesterol ester storage disease, various immune deficiencies and disorders, infectious
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes substantially purified human proteins (referred to as open reading frame, ORFX, where X is 1-11491 (see Table in the specification). ABN15762 to ABN27252 encode the human ORFX proteins given in ABP00010 to ABP11500. ORFX proteins are useful for treating or preventing a pathology associated with an ORFX-associated disorder in humans, and in the manufacture of a medicament for treating syndrome associated with ORFX-associated disorder. ORFX polynucleotide
                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequences can be used in gene therapy. ORFX sequences can be used in the treatment of cancer, hyperproliferative disorders, cirrhosis of liver, psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage, osteoarthritis, neurodegenerative disorders, disorders related to organ
                                                                                                                                                                                                                                                        systemic cytokine damage.
                                                                                                                                                                                                                                                                                                                                            useful for treating burns, incisions,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID 10760; 1037pp; English.
                                                             Local Similarity hes 6; Conserv
1 LLLVIA 6
                                                                                                                                                   93
                                                                 Conservative
                                                                                                                                                   AA;
                                                                                 100.0%;
                                                                 0
                                                             Score 24; DE
Pred. No. 3.2
0; Mismatches
                                                                                                                                                                                                                                                                                                                                            ulcers,
                                                                                                     DB
                                                                                 2e+02;
                                                                                                          23;
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                                                                                                                                                                                                                                                                                                                                            for treating osteoporosis,
                                                                                                     Length
                                                                 Indels
                                                                                                                                                                                                                part of the printed directly from WIPO
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                                                             0;
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                                                             Gaps
                                                             0
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RESULT 5
ABB90320
 24-MAY-2002
                                                         ABB90320 standard; Protein; 140 AA
(first entry)
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Human polypeptide SEQ ID NO 2696.

Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetto; antiinflammatory; antidicer; vulnerary; antionvulsant; antibacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder cardiant; gene therapy; cancer; immune disorder; neurological disease; infection; human; secreted secreted protein

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WPI; 2002-122018/16
N-PSDB; ABL90729.
                                 19-MAY-2000; 2000US-205515P
                        (HUMA-) HUMAN GENOME SCI INC
                                         18-MAY-2001; 2001WO-US16450
                                                          WO200190304-A2
                                                                  Homo sapiens
                CE,
                Rosen CA;
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ABP39430
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Best Local Similarity
Matches 6; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to novel genes (ABL89449-ABL90853) and proteins (ABB89040-ABB90444) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast; gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
              Disclosure;
                                                                                                                                                                                                                                                                                                           US6380370-B1
                                                                                                                                                                                                                                                                                                                                                                                                                  Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format dir from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                 14-AUG-1997;
08-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                   Staphylococcus
                                        Novel isolated nucleic acid encoding a Staphylococcus epidermidis polypeptide, useful for diagnosing and treating bacterial infections
                                                                                          N-PSDB; ABN91975
                                                                                                                                   Doucette-Stamm LA,
                                                                                                                                                                                                                                              13-AUG-1998;
                                                                                                                                                                                                                                                                            30-APR-2002
                                                                                                                                                                                                                                                                                                                                      Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                     antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABP39430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 11; SEQ ID NO 2696; 2081pp +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gastrointestinal, pulmonary, cardiovascular, renal and proliferative
disorders -
                                                                                                                                                                  (GENO-) GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABP39430 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           prevention of neural,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel 1405 isolated polypeptides, useful for diagnosis, treatment and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 LLLVIA 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LLLVIA 100
                                                                                                        2002-381255/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  140
              SEQ ID 4275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA;
                                                                                                                                                                  THERAPEUTICS CORP
                                                                                                                                                                                                                                                                                                                                      epidermidis
                                                                                                                                                                                                                                                                                                                                                                   gene therapy
                                                                                                                                                                                                                                                                                                                                                                                   epidermidis; open reading frame; ORF; bacterial infection;
                                                                                                                                                                                                                                                                                                                                                                                                                epidermidis ORF amino acid sequence SEQ ID NO:4275
                                                                                                                                                                                                 97US-055779P
97US-064964P
                                                                                                                                                                                                                                              98US-0134001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein; 173
                                                                                                                                     Bush
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immune system, muscular, reproductive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .0%;
            267pp; English
                                                                                                                                   D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 24;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 23;
5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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RESULT 7
ABB10539
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Best Local :
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                                                                                                                                                                                                                    18-APR-2000;
19-MAY-2000;
07-JUN-2000;
                                                                                                                                                                                                                                                      31-JAN-2000;
04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
                                                                      14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
                                                                                                                                11-JUL-2000;
11-JUL-2000;
14-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading frame (ORF) nucleic acid sequences which encode the amino acid sequences given in ABP35124 to ABP37960. The S. epidermidis sequences have antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections, particularly S. epidermidis infections. The sequences can be used to screen for compounds able to interfere with the S. epidermidis life cycle or inhibit S. epidermidis infection.

N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                        muscular disorder; reproductive disorder; gastrointestinal disorder; pulmonary disorder; cardiovascular disorder; renal disorder; proliferative disorder; inflammation.
                                                                                                                                                                    07-JUL-2000;
07-JUL-2000;
                                                                                                          26-JUL-2000;
26-JUL-2000;
                                                                                                                                                                                            28-JUN-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB10539;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABB10539 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                           17-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                   02-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                           WO200154474-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USPTO web site.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 LLLVIA 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene therapy; neural disorder; immune system disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO: 847.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     173 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
2000US-189874P.
2000US-19076P.
2000US-1915P.
2000US-205515P.
2000US-214886P.
2000US-215135P.
2000US-2151880P.
2000US-217487P.
2000US-217487P.
2000US-217487P.
2000US-217496P.
2000US-227564P.
2000US-225513P.
2000US-225513P.
2000US-225568P.
2000US-22568P.
2000US-22568P.
2000US-22568P.
2000US-22577P.
2000US-22577P.
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2000US-184664P.
2000US-186350P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                           2001WO-US01349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 24; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            179 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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RESULT 8
AAU18139
ID AAU1
XX
AC AAU1
XX
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                                                                                             В
                                                                                                                                                                                             Query Match
Best Local S
Matches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                               08-NOV-2000
08-NOV-2000
08-NOV-2000
17-NOV-2000
01-DEC-2000
01-DEC-2000
01-DEC-2000
05-DEC-2000
                                                                                                                                                                                                                            The present invention provides human cDNAs, proteins and related gen DNAs. These can be used in the treatment of neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal and proliferative disorders and inflammation. The present sequences are supported to the present sequences and proliferative disorders.
                                                                                                                                                                                                                                                                                                               Isolated nucleic acid \mathfrak n polypeptide is used in condition -
                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-476161/51.
N-PSDB; ABA06761.
           AAU18139;
                                   AAU18139 standard;
                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                         Claim 11;
                                                                                             134
                                                                                            1 LLLVIA 6
||||||
134 LLLVIA 13
                                                                                                                                                                                                                  מ
                                                                                                                                                                                                                  protein
                                                                                                                                            Similarity 6; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                          HUMAN
                                                                                                                                                                                                                                                                                         SEQ
                                                                                                                                                                                             179
                                                                                                                                                                                                                                                                                                                                                                                                                                               2000US -246609P

2000US -246611P

2000US -246613P

2000US -24920PP

2000US -24920PP

2000US -249211P

2000US -249211P

2000US -249211P

2000US -249215P

2000US -249215P

2000US -249215P

2000US -249216P

2000US -249218P

2000US -249264P

2000US -249264P

2000US -249264P

2000US -249264P

2000US -249264P

2000US -249264P

2000US -251989P

2000US -251866P

2000US -251869P

2000US -251869P

2000US -251869P

2000US -251969P

2000US -251969P

2000US -251969P

2000US -251969P

2000US -2519678P
                                                                                                                                             Conservative
                                                                                                                                                                                                                  of the
                                                                                                                                                                                                                                                                                                                                                                                                                          GENOME
                                                                                                                                                                                                                                                                                         ID NO:
                                                                                                                                                                                           ΑA;
                                                                                                                                                                                                                                                                                                                                                                                                   SC,
                                   Protein;
                                                                                                                                                                                                                   invention
                                                                                                                                                      100
                                                                                                                                                                                                                                                                                        847;
                                                                                                                                                                                                                                                                                                                                                                                                                          SCI
                                                                                                                                                                                                                                                                                                                                       molecule encoding an inflammation-associated
                                                                                                                                                                                                                                                                                                                           preventing, treating or ameliorating a
                                                                                                                                                       .0%;
                                                                                                                                                                                                                                                                                       859pp + Sequence Listing; English
                                   179
                                                                                                                                             0;
                                                                                                                                           Score 24; DE
Pred. No. 6.6
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                   SM;
                                   A
                                                                                                                                           DB 22;
6.6e+02;
hes 0;
                                                                                                                                                                  Length 179;
                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                           medical
                                                                                                                                           Gaps
                                                                                                                                                                                                                               sequence
                                                                                                                                                                                                                                                                genomic
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14-AUG-2000
114-AUG-2000
127-AUG-2000
22-AUG-2000
22-AUG-2000
23-AUG-2000
23-AUG-2000
23-AUG-2000
23-AUG-2000
23-AUG-2000
24-AUG-2000
25-SEP-2000
25-SEP-2000
26-SEP-2000
27-SEP-2000
28-SEP-2000
28-SEP-2000
28-SEP-2000
29-SEP-2000
21-SEP-2000
22-SEP-2000
23-SEP-2000
24-SEP-2000
25-SEP-2000
26-NOV-2000
27-SEP-2000
28-NOV-2000
29-SEP-2000
29-SEP-2000
20-NOV-2000
20-N

2000US-22575PP 2000US-22575PP 2000US-22575PP 2000US-2256668P 2000US-2256668P 2000US-2256668P 2000US-2256668P 2000US-225934PP 2000US-225934PP 2000US-225934PP 2000US-225934PP 2000US-23112443P 2000US-23112443P 2000US-2311414P 2000US-2311414P

0;

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RESULT 9
AAU18690
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
11-DEC-2000;
05-JAN-2001;
31-JAN-2000; 2000US-0179065.
04-FEB-2000; 2000US-0180628.
                                                                                                                                                                                   Human; antiinflammatory; neuroprotective; immunomodulator; vulnerary; cardiovascular; cytostatic; nephrotropic; antianaemic; nephritis; immunosuppressive; kidney disorder; renal failure; hypertension; cardiovascular disorder; myocardial infarction; blood disorder; anaemia blood coagulation disorder; electrolyte imbalance disorder; cancer; hyponatraemia; hyperkalaemia; neoplastic disorder; nephtoma; autoimmune disease; inflammatory disease; reproductive system disorder; autoimmune disease; nephtomatory disease; reproductive system disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to the isolation of novel human uterine motility-association polypeptides, and cDNA (AAS28936-AAS: and genomic sequences encoding for these polypeptides. The sequences of the invention are useful in the diagnosis, treatment, prevention and/or prognosis of diseases associated with uterine motility such as pregnancy and labour, and menstrual disorders. The polynucleotide sequences of the invention are also useful in gene therapy. AAU18094-AAU18152 represent novel human
                                          17-JAN-2001; 2001WO-US01359
                                                                                                                                                                                                                                                                                                                                                                   AAU18690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isolated polypeptide and nucleic acid molecules for treating, preventing and/or prognosing disorders related to uterine motility e.g. disorders associated with pregnancy and the menstrual cycle -
                                                                                                    WO200155328-A2
                                                                                                                                 Homo
                                                                                                                                                      autoimmune disease; inflammatory disease; reproductive systendocrine disorder; neural activity; neurological disorder; wound healing; respiratory disorder.
                                                                                                                                                                                                                                                                                                                                      21-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                              AAU18690 standard; Protein; 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          uterine motility-association polypeptides.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                          Renal and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAS28981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     134 LLLVIA 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 LLLVIA 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                               sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2001-488777/53.
                                                                                                                                                                                                                                                                                                       cardiovascular-associated protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID No 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; 2000US-0251869.
; 2000US-0251989.
; 2000US-0251990.
; 2000US-0254097.
; 2000US-0259678.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ą,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 24;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NS.
                                                                                                                                                                                                                                                                                                                                                                                              AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB
                                                                                                                                                                                                                                                                                                       Seq ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 179;
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                                                                                                                                                                                                                                                                                                        129.
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                                                                                                                                                                                                                                 anaemia;
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   14-AUG-2000

18-AUG-2000

18-AUG-2000

22-AUG-2000

22-AUG-2000

23-AUG-2000

23-AUG-2000

01-SEP-2000

01-SEP-2000

01-SEP-2000

01-SEP-2000

05-SEP-2000

06-SEP-2000

08-SEP-2000

08-SEP-2000
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14-SEP-2000
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14-SEP-2000
14-SEP-2000
14-SEP-2000
14-SEP-2000
21-SEP-2000
21-SEP-2000
25-SEP-2000
25-SEP-2000
27-SEP-2000
27-SEP-2000
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29-SEP-2000
29-SEP-2000
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11-JUL-2000;
11-JUL-2000;
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19-MAY-2000;
07-JUN-2000;
28-JUN-2000;
30-JUN-2000;
07-JUL-2000;
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02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
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26-JUL-
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2000US-0231242
2000US-0231243
2000US-0231244
2000US-0231244
2000US-0231413
2000US-0231413
                                       2000US-0235834.
2000US-0235836.
2000US-0236327.
2000US-0236367.
2000US-0236368.
2000US-0236369.
2000US-0236370.
                                                                                                                                          2000US-0234274.
2000US-0234997.
2000US-0234998.
2000US-0235484.
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2000US-0233065.
2000US-0234223.
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2000US-0232400.
2000US-0232401.
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2000US-0231968.
2000US-0232397.
2000US-0232398.
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2000US-0227009.
2000US-0228924.
2000US-0229287.
2000US-0229343.
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2000US-0229513.
2000US-0230437.
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2000US-0186350.
2000US-0189874.
2000US-0190076.
2000US-0198123.
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2000US-0229345
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2000US-0226279
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2000US-0225757
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2000US-0225270
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2000US-0225213
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05-DEC
       New polynucleotides and polypeptides, useful for diagnosing, treating, preventing or prognosing e.g. kidney, cardiovascular, blood, electrolyte imbalance or neoplastic disorders, autoimmune diseases,
                                                                                         Rosen
                                                       N-PSDB;
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17-NOV-2000;
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DB; AAS30211.
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2000US-0249212
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RESULT 10
AAU17055
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Matches 6
16-MAR-2000;
17-MAR-2000;
18-APR-2000;
19-MAY-2000;
07-JUN-2000;
28-JUN-2000;
30-JUN-2000;
07-JUL-2000;
07-JUL-2000;
                                                                                                                                    31-JAN-2000;
04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        electrolyte imbalance disorders (e.g. hyponatraemia or hyperkalaemia), neoplastic disorders (e.g. nephtoma or renal cell cancer), autoimmune diseases, cancers, inflammatory diseases, reproductive system disorders, endocrine disorders, neural activity and neurological disorders, wound healing and respiratory disorders. AAU18644-AAU18715 represent the novel human renal and cardiovascular associated amino
                                                                                                                                                                                                                                                                                                                                                                               cytostatic; cardiant; vasotropic; cerebroprotective; neuroprotective; antibacterial; vincide; fungicide; vulnerary; secreted protein; rheumatoid arthritis; hyperproliferative disorder; cardiovascular disorder; cerebrovascular disorder; cerebral ischaemia; angiogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                did not form part of the printed specification, but was obtained electronic format directly from WIPO at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to novel nucleic acids and polypeptides useful for diagnosing, treating, preventing and/or prognosing disorders related to these polypeptides. The polypucleotides are especially useful in the diagnosis, prognosis, prevention and/or treatment of diseases which include kidney disorders (e.g. renal failure or nephritis), cardiovascular disorders (e.g. hypertension or myocardial infarction), blood disorders (e.g. anaemia or blood coagulation disorders).
                                                                                                                                                                                                                                                                                                                                                   cerebrovascular disorder; cerebral ischaemia; angiogenesis; nervous system disorder; Alzheimer's disease; infection; ocular corneal infection; wound healing; epithelial cell proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-NOV-2001
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                                                                                                                                                                                                                                                                                                        Homo sapiens.
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 2000US-0189874.

2000US-019076.

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2000US-0186350
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                                                                                                                                                                                                                                                                                                                                     additive; preservative; antiproliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein; 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein,
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opthalmalogical;
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017-NOV-2000
17-NOV-2000
17-NO
The invention relates to isolated nucleic acid molecules and their encoded secreted proteins. The nucleic acids and proteins are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a pathological condition. Antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme linked
                                                                                                                                                                                                   Novel polypeptides and polynucleotides useful as diagnostic reagents diagnose diseases or disorders associated with aberrant expression or activity of polypeptides, for treating blood clotting disorder, haemophilia
                                                                                                                                                                                                                                                                                                WPI; 2001-476222/51.
N-PSDB; AAS26960.
                                                                                                                                                                     Claim
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2000US-023349.
2000US-023399.
2000US-023399.
2000US-023399.
2000US-0234778.
2000US-0241786.
2000US-0241786.
2000US-0241808.

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RESULT 11
AAG10813
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    CC immunosorbant assays (ELISA). Disorders which are diagnosed or treated CC include autoimmune diseases e.g. rheumatoid arthritis, CC hyperproliferative disorders e.g. neoplasms of the breast or liver, CC cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, reprove system disorders e.g. CC Alzheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection, and many other can also CC alzheimer's listed in the specification. The polypeptides can also CC be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, confactors and other nutritional components. The present
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      termination sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter
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Pred. No. 6.6e+02;
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99US-0140653

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Similarity 100.0%;
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99US-0121825
99US-0125548
99US-0125788
99US-0125785
99US-0126785
99US-0128714
99US-0128714
99US-0130077
99US-0130491
99US-01314491
99US-01344211
99US-0134421
99US-0134470
99US-0134421
99US-0134471
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99US-0161359.
99US-0161361.
99US-0161361.
99US-0161920.
99US-0161993.
99US-0162142.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 24; DB 21;
Pred. No. 6.7e+02;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pathway;
promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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27-JUL-1999
28-JUL-1999
28-JUL-1999
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29-AUG-1999
20-AUG-1999
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27-AUG-1999
28-SEP-1999
29-SEP-1999
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28-SEP-1999
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25-AUG-1999
26-AUG-1999
27-AUG-1999
27-AUG-1999
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29-AUG-1999
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21-AUG-1999
21-AUG

990S-0145918
990S-0145918
990S-0146386
990S-0146388
990S-0147038
990S-0147192
990S-0147192
990S-0147192
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990S-0147193
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990S-0148171
990S-0151081
990S-0159338
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9US-016081 9US-016081 9US-016098 9US-016198 9US-016140 9US-016146 9US-016136 9US-016136 9US-016136 9US-016136 9US-016136	908-0158232 908-0158232 908-0158233 908-0159294 908-0159294 908-015933 908-015933 908-015933 908-015933 908-0159637 908-0160767 908-0160767	99US-0149902 99US-0149930 99US-015086 99US-0151086 99US-0151080 99US-01511080 99US-01511080 99US-0151133 99US-0151363 99US-015363 99US-0153638 99US-0153638 99US-0154018 99US-0154018 99US-015659 99US-015659 99US-0156596 99US-0156596 99US-0156596	9US-014720 9US-014730 9US-014717 9US-014717 9US-014741 9US-014741 9US-01474 9US-01474 9US-014817 9US-014834 9US-014834 9US-014834 9US-014834 9US-014834 9US-014834

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RESULT 13
AAG10812
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Best Local S
Matches 6
25-FEB-1999

05-MAR-1999

09-MAR-1999

23-MAR-1999

24-MAR-1999

01-APR-1999

01-APR-1999

01-APR-1999

01-APR-1999

16-APR-1999

23-APR-1999

23-APR-1999

23-APR-1999

23-APR-1999

23-APR-1999

24-MAY-1999

05-MAY-1999

06-MAY-1999

07-MAY-1999

11-MAY-1999

14-MAY-1999

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana protein fragment SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-OCT-1999;
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|11 LLLVIA 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 24; DE clarity 100.0%; Pred. No. 6.7 Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000EP-0301439
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 99US-0125788
99US-0125788
99US-0125788
99US-0126785
99US-0126785
99US-0129845
99US-0130449
99US-0130510
99US-0132484
99US-0132484
99US-0132487
99US-0132487
99US-0134278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 21;
6.7e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 182;
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14-JUN-1999;
16-JUN-1999;
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17-JUN-1999
99US-0138540
99US-0139119
99US-0139119
99US-0139159
99US-0139450
99US-0139450
99US-0139450
99US-0139460
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99US-0145913
99US-0146388
99US-0146388
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99US-0147302
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99US-0147302
99US-0146388
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Query Match
Best Local S
Matches 6
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11-AUG-1999
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24-AUG-1999
27-AUG-1999
28-EEP-1999
29-EEP-1999
29-EEP-1999
29-EEP-1999
29-EEP-1999
20-CCT-1999
20-CCT-1999
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11-OCT 1999
21-OCT 1999
21-OCT 1999
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     1 LLLVIA 6
                                        Similarity 6; Conserv
                                        100.0%;
ilarity 100.0%;
Conservative (
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99US-0148311
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99US-0148311
99US-0148313
99US-0149326
99US-0149223
99US-0149223
99US-0151065
99US-0151065
99US-0151065
99US-0151065
99US-0151065
99US-0151080
99US-0160814
99US-0160814
99US-0160814
99US-0160815
99US-0160815
99US-0160815
99US-01610815
99US-0161109
                                        0;
                                                     Score 24; DB 21;
Pred. No. 6.8e+02;
                                        Mismatches
                                                                     Length 183;
                                      Indels
                                      0;
                                    Gaps
                                      0;
 RESULT 14

AAG42629

ID AAG42629

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XX AAG42629

XX AAG42629

XX AAG42629

AC AAG42

XX Prot

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PR 06-:

PR 29-
PR 29
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05-MAR 1999
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23-MAR 1999
25-MAR 1999
26-MAR 1999
27-MAR 1999
28-MAR 1999
16-APR 1999
08-APR 1999
08-APR 1999
28-APR 1999
21-APR 1999
21-MAY 1999
11-MAY 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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| LLLVIA 17
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990S-0121825
990S-0123788
990S-0125788
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990S-0126786
990S-012824
990S-0128214
990S-013091
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990S-0132848
990S-0132863
990S-0134216
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990S-0134272
990S-0134272
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990S-013427
990S-0135782
990S-0136782
990S-013623
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RESULT 15
AAU45545
ID AAU45
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Best Local S
Matches 6
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18-AUG-1999
20-AUG-1999
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21-AUG-1999
23-AUG-1999
25-AUG-1999
25-AUG-1999
27-AUG-1999
28-SEP-1999
29-SEP-1999
20-SEP-1999
21-CCT-1999
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AAU45545
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6; Conserv
 standard;
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nilarity 100.
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99US-0149723.
99US-0149723.
99US-0149923.
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99US-0161361.
 Protein;
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  271
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                                                                                            Score 24; DB 21;
Pred. No. 6.8e+02;
); Mismatches 0;
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                                                                                                              Length
                                                                                             0
                                                                                             Gaps
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18-JUN-1999
19-JUN-1999
19-JUN

9908-0139455.
9908-0139458.
9908-0139461.
9908-01339463.
9908-0139463.
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                                                                                                                                                                                nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA).

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fire wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central
                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 3; SEQ ID No 6740; 1069pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-616774/71.
N-PSDB; AAS59526.
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02-JUN-2000; 2000US-208841P.
07-JUL-2000; 2000US-216747P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             treating acne vulgaris
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LLLVIA 52
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, Jen S, Carter D;
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                                                                          Mismatches
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Search completed: January 3, 2003, 15:28:38 Job time: 27.5909 secs

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Copyright (c) 1993 - 2003 Compus
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core 24; DB 2; Len red. No. 2.2e+02; Mismatches 0: T	RESULT 2 F43594 15K cysteine-rich outer membrane protein - Chlamydia trac C; Species: Chlamydia trachomatis C; Species: Chlamydia trachomatis C; Date: 12-Jan-1993 *text_ C; Accession: F43584; S24274 R; de la Maza, L.M.; Fielder, T.J.; Carlson, E.J.; Markoff Infect. Immun. 59, 1196-1201, 1991 A; Tille: Sequence diversity of the 60-kilodalton protein A; Reference number: A43584; MUID:91147205; PMID:1997423 A; Accession: F43584 A; Status: prelininary A; Molecule type: DNA A; Residues: 1-152 A; Cross-references: EMBL:X54388; NID:940760; PIDN:CAA3825 C; Superfamily: Chlamydia 15K cysteine-rich outer membrane C; Keywords: membrane protein	Query Match 100.0%; Score 24; DB 2; Len Best Local Similarity 100.0%; Pred. No. 2.1e+02; Matches 6; Conservative 0; Mismatches 0; I Qy 1 LLLVIA 6	RESULT 1 C71515 C71515 C71515 C;Species: Chlamydia trachomatis C;Species: Chlamydia trachomatis C;Species: Chlamydia trachomatis C;Accession: C71515 R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Mara Science 282, 754-759, 1998 A;Title: Genome sequence of an obligate intracellular pat A;Reference number: A71570; MUID:99000809; pMID:9784136 A;Accession: C71515 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-150 <arn> A;Cross-references: GB:AE001317; GB:AE001273; NID:9332886 A;Experimental source: serotype D, strain UM-3/Cx C;Genetics: A;Gene: crpA C;Superfamily: Chlamydia 15K cysteine-rich outer membrane</arn>	ALIGNMENTS	30 24 100.0 509 2 A57512 31 24 100.0 650 2 E95296 32 24 100.0 654 2 G84153 32 24 100.0 726 2 S50833 34 24 100.0 770 2 T00204 35 24 100.0 770 2 T00204 36 24 100.0 896 2 AB1156 37 24 100.0 896 2 AB1156 38 24 100.0 1011 2 T45718 38 24 100.0 1011 2 T45718 39 24 100.0 1239 2 T42020 40 24 100.0 1239 2 T42020 41 23 95.8 73 2 AB3444 42 23 95.8 73 2 AB3444 43 23 95.8 100 2 T43116 44 23 95.8 100 2 T43116 45 23 95.8 100 2 T43116
ngth 152;	trachomatis (serotype C) text_change 10-Dec-1999 rkoff, B.A.; Peterson, E.M. tein and of a putative 15-kilodal 423 A38258.1; PID:g40762 brane protein	ngth 150; Indels 0; Gaps 0;	chomatis (serotype D, strain UW3/text_change 10-Dec-1999 Marathe, R.; Aravind, L.; Mitche r pathogen of humans: Chlamydia t 136 328863; PIDN:AAC68041.1; PID:g332		beta-glucosidase B probable ARC-type hypothetical prote holocarboxylase sy LDL receptor relat LDL receptor relat conserved membrane conserved membrane receptor-kinase li class IV chitin sy hypothetical prote gp38 protein - Myc hypothetical prote hypothetical prote probable membrane hypothetical prote probable membrane

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Xperimental source: strain pasc
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H.
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.;
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigu Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y., F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A., F.G.; Nunes, L.R.; Oliveira, M.A.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak A;Authors: da Silva, A.C., da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira, M.C.; de Sa, R.G.; Santelli, R.V.; Sawasak A;Authors: da Silva, A.C., da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira, M.C.; de Sa, R.G.; Santelli, R.V.; Sawasak A;Authors: da Silva, A.C., da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira, M.C.; de Sa, R.G.; Santelli, R.V.; Sawasak A;Authors: da Silva, A.C., da Silva, F.R.; da Silva, S.; Vettore, A.L.; Z
                                                                                                                                                                                                                    A;Cross-references:
C;Genetics:
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A; Residues: 1-183 <S'
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A;Accession: G84609
A;Status: preliminary
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R;anonymous, The Xylella fastidiosa Consortium of the Organization for N Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa. A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below A;Accession: D82812
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                                                                                                                                                                                                                                                                                                                                                                               A; Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana A; Reference number: A84420; MUID:20083487; PMID:10617197
                                                                                                                                                                                                                                                                                                                                                                                                                                   euss, D.; Nierman, W.C.; Nature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Contents: annotation C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               M.; Tsuhako, M.H.; Vallada, H.;
A;Reference number: A59328
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                                                                                                                                                                  Gene: At2g22170
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Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
Accession: G84609
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L. Ss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
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R; Davidson, S.;
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probable integral membrane protein - Streptomyces coelicolor (;Species: Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_char C;Accession: T36065
R;Saunders, D.C.; Harris, D.; Bentley, S.D.; Parkhill, J.; Be submitted to the EMBL Data Library, November 1998
A;Reference number: Z21595
A;Accession: T36065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C;Accession: C72609
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A;Introns: 42/1; 93/3; 141/3; 188/2
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A;Cross-references: EMBL:AF022977; PIDN:AAB88611.1; GSPDB:GN00023; CESP:ZK994.4
A;Experimental source: strain Bristol N2; clone ZK994
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C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
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A; Experimental source: strain K1
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A; Residues: 1-232 <KAW>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           awa, H.; Takamiya, M.; Masuda,
DNA Res. 6, 83-101, 1999
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||||||
82 LLLVIA 87
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hypothetical protein C54H2.5 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct.1999 #sequence_revision 15-Oct.1999 #text_change C;Accession: T29611
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R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N. o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuc DNA Res. 3, 109-136, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: The atpl and atp2 operons of the cyanobacterium Synechocystis sp. A;Reference number: S17745; MUID:92003679; PMID:1832989 A;Accession: S17746
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C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change C;Accession: S17746; S74588; S14861
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A; Cross-references: EMB
 submitted to the EMBL Data
                    R; Fulton,
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A; Residues: 1-276 < KAN>
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A; Residues: 1-276 <L:
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7-44/Domain: transmembrane #status predicted <TM1>
63-82/Domain: transmembrane #status predicted <TM2>
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lternate names: ATP synthase chain a
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Library, May 1996
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Pred. No. 3.1
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Pred. No. 3.5
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3.1e+02;
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C;Species: Pseudomonas fluorescens
C;Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #tex:
C;Accession: S22414
R;Black, M.T.; Munn, J.G.R.; Allsop, A.E.
Blochem. J. 282, 539-543, 1992
Blochem. J. 282, 539-543, 1992
A;Title: On the catalytic mechanism of prokaryotic leade
A;Reference number: S22413; MUID:92189595; PMID:1546969
A;Accession: S22414
                                                     A; Molecule type: DNA
A; Residues: 1-284 <BLA>
A; Residues: 1-284 <BLA>
A; Cross-references: EMBL: X56466; NID: 945509; PIDN: CAA39839.1;
C; Superfamily: signal peptidase I
C; Keywords: hydrolase; serine proteinase; transmembrane protei
                                                                                                                                                                                                                                                                                                                                        signal peptidase I (EC 3.4.21.89) - N; Alternate names: leader peptidase
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A; Residues: 1-281 <KAN>
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A;Accession: S74551
A;Status: preliminary
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A; Introns: 23/3; 126/2;
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A;Experimental source: strain Bristol N2; clone C54H2
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A; Residues: 1-277 < FUL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; IR. Res. 3, 109-136, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  264 LLLVIA
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les 6; Conser
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Score 24;
Pred. No.
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Pred. No.
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  3.6e+02;
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                  Length 284;
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                                                          protein
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                                                                                                                                                                                                                   peptidase
                                                                                                   PID:g45511
                                                                                                                                                                                                                                                                                                    19-May-2000
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RESULT 14
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Best Local Similarity
6; Conserva
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C;Superfamily: signal peptidase I
C;Keywords: hydrolase; serine proteinase
:Species: Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                                                   A;Molecule type: DNA
A;Residues: 1-295 <KUR>
A;Cross-references: GB:AE007870; PIDN:AAK89937.1; PID:g15159892; GSPDB:GN00170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical ABC transporter permease protein yddQ AGR_L_2741 [imported] - Agrobacterium C;Species: Agrobacterium tumefaciens C;Date: 22-Oct_2001 #sequence_revision 22-Oct-2001 #text_change 11-Jan-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable signal peptidase I (EC 3.4.21.89) PA0768 [similarity] - Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 24-May-2001
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                             ABC transporter, membrane spanning protein
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A;Reference number: A82950; MUID:20437337; PMID:10984043
Accession: H83550
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                                                                                                                                                                                                                                                                                                             Genetics:
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Molecule type: DNA
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ilarity 100.0%;
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                                                                                                                                                                                     100.0%; Score 24; DB 2; 100.0%; Pred. No. 3.7e+02; O. Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                     the Plant Pathogen and Biotechnology Agent Agrobacterium tun PMID:11743194
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Pred. No. 3.6e+02;
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                              Atu3458 [imported]
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                             Agrobacterium
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Larbig,
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Markelz, B.
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K.; Lim,
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2003, 15:33:17

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R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McCl; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kam ster, E.W.
                                                                      Query Match
Best Local Similarity
6; Conserv
                                                                                                                                                                                                  A; Gene: YPO2507
                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-295 <KUR>
A; Cross-references: GB:AL590842;
                                                                                                                                                                                                                                                                                                                                                 A; Reference number: AB0001; A; Accession: AD0306
                                                                                                                                                                                                                                                                                                                                                                        A; Title: Genome sequence of Yersinia pestis, the causative agent of plague. A; Reference number: AB0001; MUID:21470413; PMID:11586360
                                                                                                                                                                                                                                                                                                                                                                                                                       R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G. il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrel Nature 413, 523-527, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable membrane protein YPO2507 [imported] - Yersinia pestis (strain CO92) C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001 C;Accession: AD0306
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Best Local Similarity
...thas 6; Conserva
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A;Cross-references: GB:AE008689; PIDN:AAL44271.1; PID:g17741857; GSPDB:GN00187
A;Experimental source: strain C58 (Dupont)
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A; Accession: AI2981
A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                         A; Status: preliminary
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Pred. No. 3.7e+02;
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Pred. No. 3.7e+02;
Mismatches 0;
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Maximum DB :
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Maximum Match 100%
Listing first 45 summaries
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"Bacteriophage T4 genome analysis.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
                                                                  between
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Science 282:754-759(1998).
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                                                                                                                                                                                                                Matches
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Best Local (
                                               Y096_GVCL
P41728;
01-NOV-1995
01-NOV-1995
15-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it
                                                                                                                                                                                                                                                                                                                                                                                                                                               15-kilodalton protein between the trachoma and venereum blovars of Chlamydia trachomatis.";
Infect Immun. 59:1196-1201(1991)
-i- FUNCTION: ASSOCIATED WITH DIFFERENTIATION C (RBS) INTO ELEMENTARY BODIES (EBS). IT IS N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CRPC_CHLTR STANDARD; PRT; 152 AA. P26756; P26756; O1-AUG-1992 (Rel. 23, Created) O1-BUG-1992 (Rel. 23, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) 15 kDa cysteine-rich outer membrane protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE001317; AAC68041.1;
Outer membrane; Complete pro
SEQUENCE 150 AA; 15985 M
                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=91147205; PubMedede la Maza L.M., Fiedler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chlamydia trachomatis. Bacteria; Chlamydiales;
                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                       PIR; F43584; F43584.
                                                                                                                                                                                                                                                                                                  EMBL; X54388; CAA38258.1;
                                                                                                                                                                                                                                                                                                                           or send an
                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=C/TW-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CRPA
                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SUBCELLULAR LOCATION: Outer membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peterson E.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=813;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence diversity of the 60-kilodalton protein and of a putative
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48 LLLVIA 53
                                                                                                                                                                                       1 LLLVIA 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                     (RBS) INTO ELEMENTARY BODIES (EBS).
INTEGRITY OF THE EBS OUTER ENVELOPE.
                                                                                                                                                                                                                                                              membrane.
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                                     (Rel. 32, (Rel. 32, (Rel. 37, 18.6 kDa)
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                                                                                                                                                                                                              Conservative
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                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=1997423;
                                                                                                                                                                                                                                                              16133 MW;
Createu,
Last sequence update,
Last annotation update)
a protein in P143-LEF5 intergenic region.
~~~nulosis virus (CIGV) (Cryptophlebia
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                                                                                                                                                                                                             Score 24; DE Pred. No. 1.2 0; Mismatches
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Pred. No.
                                                                                                                                                                                                                                                              31D325CC0619A2F1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77A6FB7CC8FADB34 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                                                                                                                    (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chlamydia
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NECESSARY FOR STRUCTURAL
                                                                                                                                                                                                                                                                                                                                                           its content
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Cryptophlebia Hypothetical

leucotreta granulosis

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RESULT 6
ATP6_SYNY3
ID ATP6_S
AC P27178
AC P27178
AC P1-AUG
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DE ATP SY
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Best Local S
Matches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATP6_SYNY3 STANDARD; PRT; 276 AA. P27178; 01-AUG-1992 (Rel. 23, Created) 01-AUG-1992 (Rel. 23, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) ATP Synthase A chain (EC 3.6.3.14) (Protein 6). ATPB OR ATPI OR SLL1322.
                                                                                                                                                                                                                                  Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y., Miyajima N., Hirosawa M., Sujurra M., Sasamoto S., Kimura T., Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruc K., Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M., Tabata S.; Yamada M., Yasuda M., Tabata S.; "Squence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Genome organization of the DNA-binding protein gene region of Cryptophlebia leucotreta granulosis virus is closely related to of nuclear polyhedrosis viruses.";

J. Gen. Virol. 75:1815-1820(1994).

-!- SIMILARITY: TO CORRESPONDING ORF IN ACMNPV AND OPMNPV.

-!- CAUTION: IT IS UNCERTAIN WHETHER MET-1 IS THE INITIATOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical SEQUENCE 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=97061201; PubMed=8905231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE=92003679;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synechocystis sp. (strain PCC 6803).
Bacteria; Cyanobacteria; Chroococcales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X77048; CAA54340.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The atpl and atp2 operons of the cyanobacterium Synechocystis sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=1148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Genome organization of the DNA-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jehle J.A., Backhaus
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                               H(+)(Out).
SUBUNIT: F.
CORE - AND
                                                                                                               FUNCTION: KEY COMPONENT OF THE PROTON CHANNEL; IT MADIRECT ROLE IN THE TRANSLOCATION OF PROTONS ACROSS CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) = ADP +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6803
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|LLLVIA 14
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                                                                                                                                                                                                               3:109-136(1996)
                               T: F-TYPE ATPASES HAVE 2 C
AND CF(0) - THE MEMBRANE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17:641-652(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=1832989;
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                            HAVE 2 COMPONENTS, CF(1) - TH MEMBRANE PROTON CHANNEL. CF(1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 24;
Pred. No.
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GAMMA(1), DELTA(1),
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                                                                                                                                                                                     IT MAY PLAY A
                               THE CATALYTIC (1) HAS FIVE
                                                                                                                     phosphate
                                                                                                                                               THE MEMBRANE
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          _CAEEL
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TRANSMEM
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditidae; Peloderinae; Caenorhabditis. NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSMEM TRANSMEM
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                                                                                                                                                                                                                              Fulton L.
                                                                                                                                                                                                                                                                                                                                                             STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Armes N.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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    -!- SIMILARITY: BELONGS TO THE SURF4 FAMILY.

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Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,

A Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,

Ra Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,

Ra Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,

Ramith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

Ramith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

Reizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.;

"Complete genome sequence of Pseudomonas aeruginosa FAOI, an

"Complete genome sequence of Pseudomonas aeruginosa FAOI, an

"Popportunistic pathogen.";

"Lature 406:959-964(2000).

"I Nature 406:959-964(2000).

"I SUNCELLULAR LOCATION: Type II membrane proctein. Inner membrane.

"I SINILARITY: BELONGS TO PEPTIDASE FAMILY S26; ALSC KNOWN AS TYPE
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                                                         the European Bioinformatics Institute of Bioinformat use by non-profit institutions as long modified and this Statement is not removed. entitles requires a license agreement 'or send an email to 'license agreement' '
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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Signal peptidase I (EC 3.4.21.89) (Spase I) (
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      EMBL;
                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Electron of the Swiss Institute of Bioinformatics and the Bioinformatics
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MEDLINE-20437337; PubMed-
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Bacteria; Proteobacteria; gamma
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InterPro; IPR002995; Surf4.
Pfam; PF02077; SURF4; 1.
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InterPro: IPR000223; SigPTase_S26A.
Pfam: PF00461; Peptidase_S26; 1.
PRINTS; PR00727; LEADERPTASE.
PROSITE; PS00501; SPASE_I_1; 1.
PROSITE; PS00760; SPASE_I_2; 1.
PROSITE; PS00761; SPASE_I_3; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 secreted and periplasmic proteins precursor.
-i- SUBCELLULAR LOCATION: Type II membrane protein. Inner membrane
-i- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S26; ALSO KNOWN AS TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=92189595; PubMed=1546969;
Black M.T., Munn J.G.R., Allsop A.E.;
"On the catalytic mechanism of prokaryotic leader peptidase
Biochem. J. 282:539-543(1992).
-i- CATALYTIC ACTIVITY; Cleavage of N-terminal leader sequen
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01-NOV-1995 (Rel.
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InterPro; IPR000223; SigPTase_S26A.
Pfam; PF00461; Peptidase_S26; 1.
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                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI
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Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
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Mol. Microbiol. 28:403-412(1998).
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SUBCELLULAR LOCATION: Integral membrane
SIMILARITY: BELONGS TO THE NRAMP FAMILY.
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Length 415;
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                                                                                                                                                                                                                                                                                        a collaboration -
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HITTHER REPORTED THE PROPERTY OF THE PROPERTY 
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MNTH_MYCTU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δÃ
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Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=98295987; PubMed=9634230; Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Bavies R., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence."; Nature 393:537-544(1998).
  TRANSMEM TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restruce by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       laboratory strains.";
Submitted (APR-2001) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L., Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Probable manganese transport protein mntH MNTH OR RV0924C OR MT0951 OR MTCY21C12.18C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          005916;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=H37Rv;
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                                                                                 Transport;
                                                                                                                                                                                    Pfam; PF01566; Nramp;
                                                                                                                                                                                                                                        TubercuList; Rv0924c;
                                                                                                                                                                                                                                                                TIGR; MT0951;
                                                                                                                                                                                                                                                                                         EMBL; AE006981; AAK45198.1;
                                                                                                                                                                                                                                                                                                                    EMBL; Z95210;
                                                                                                                                                                                                                                                                                                                                                                                                                         modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bishai W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycobacterium tuberculosis
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15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                      TRANSMEM
                                                                                                                                   rigrfams;
                                                                                                                                                              ProDom; PD001861;
                                                                                                                                                                                                                  InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: BELONGS TO THE NRAMP FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   168 LLLVIA 173
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                                                                                                                                   TIGR01197; nramp;
                                                                                                                                                                                                            IPR001046; Nramp.
  Symport;
33
60
114
136 1
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                                                                                                                                                                                                                                                                                                                       CAB08494.1;
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                                                                                                                                                              Nramp; 1.
; Manganese;
53 po
80 po
134 po
156 po
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); Mismatches
                                                                               POTENTIAL.
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                                                                                                       Transmembrane;
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hes 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ΑA
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Best Local S
Matches 6
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       _PORPU
                                              HOFE_HAEIN STANDARD; PRT; 464 AA. P462; Ol-NOV-1995 (Rel. 32, Created) Ol-NOV-1995 (Rel. 32, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P51363;
01-OCT-1996
01-OCT-1996
15-DEC-1998
                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBI outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
             Bacteria;
                     Protein transport protein hofB HOFB OR HOPB OR HI0298. Haemophilus influenzae.
                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                   Chloroplast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSMEM TRANSMEM
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TRANSMEM
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Haemophilus
                                                                                                                                                                                                                                                            EMBL; U38804; AAC08249.1;
                                                                                                                                                                                                                                                                                                                                                                                         genome
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Reith M.E., Munholland J.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Rhodophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Porphyra purpurea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical
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                                                                                                                                                                                              Local Similarity
nes 6; Conserv
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                                                                                                                                                                        1 LLLVIA 6
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                                                                                                                                                                                                                                                                                                                                                                  nt Mol. Biol. Rep. 13:333-335(1995).
SIMILARITY: BELONGS TO THE YCF44 FAMILY.
                                                                                                                                                     LLLVIA 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
            Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                  nucleotide sequence of the Porphyra purpurea chloroplast
                                                                                                                                                                                                                                        437
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210
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299
323
365
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1 50.2
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34, Last sequence update)
37, Last annotation update)
kDa protein ycf44 (ORF437).
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230
278
319
343
385
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            gamma
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Pred. No.
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Pred. No. 2
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                                           homolog
                                                                                                                                                                                                                                       59F02A977B3A1BD9 CRC64;
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                                                                                                                                                                                             Mismatches
           subdivision; Pasteurellaceae;
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Best Local S
Matches 6
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P50747; Q99451;
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Biottin--protein ligase (EC 6.3 4.-) (Biotin apo-protein ligase)
[Includes: Biotin--[methylmalonyl-CoA-carboxyltransferase] ligase
(EC 6.3 4.9); Biotin--[propionyl-CoA-carboxylase (ATP-hydrolyzing]]
ligase (EC 6.3 4.10) (Holocarboxylase synthetase) (HCS);
Biotin--[methylcrotonoyl-CoA-carboxylase] ligase (EC 6.3.4.11);
Biotin--[acetyl-CoA-carboxylase] ligase (EC 6.3.4.11);
"Nikawa N., Matsubara Y., Narisawa "Isolation and characterization of holocarboxylase synthetase cDNA."; Nat. Genet. 8:122-128(1994).
                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae. NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00437; GSPII_E; 1.

ProDom; PD000739; GSPII_E; 1.

PROSITE; PS00662; T2SP_E; 1.

PROSITE; PS00662; T2SP_E; 1.

Transport; ATP-binding; Complete proteome.

NP_BIND 264 271 ATP (POTENTIAL).

SEQUENCE 464 AA; 52983 MW; 4923156BE45BD6A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                              Suzuki Y., Aoki Y.,
                                                                                                                                                           MEDLINE-95144167;
                                                                                                                                                                                               TISSUE=Liver;
                                                                                                                                                                                                                         SEQUENCE FROM N.A., AND VARIANT HCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U32715; AAC21962.1; -. TIGR; HI0298; -.
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                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=Rd / KW20 / ATCC 51907;
MEDLINE=95350630; PubMed=7542800;
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STRAIN=Rd / KW20 / ATCC 51907;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Science 269:496-512(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001482; GSPII_E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=727;
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nes 6; Conserv
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                                                                                                                                                           PubMed=7842009;
                                                                                                                           Ishida
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Pred. No. 3.1e+02;
Mismatches 0;
                                                                                                                       Chiba Y., Iwamatsu A., Kishino
                                                                mutations in
                                                                                                                                                                                                                         PRO-237
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                                                                                                                                                                                                                                                                                                                   Hominidae;
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                                                                                                                                                                                                                                                                                                                                                    Euteleostomi;
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[2]
SEQUENCE FROM N.A.
Ohira M., Seki N., N
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MEDLINE-96125714; PubMed-8541348;
AOKi Y., Suzuki Y., Sakamoto O., Li X., Takahashi K., Chtake A
AOKi Y., Suzuki Y., Sakamoto O., Li X., Takahashi K., Chtake A
Sakuta R., Ohura T., Miyabayashi S., Narisawa K.;
Sakuta R., Ohura T., Miyabayashi S., Narisawa K.;
"Molecular analysis of holocarboxylase synthetase deficiency:
"Molecular analysis of holocarboxylase synthetase deficiency:
                                                                             MEDLING-yourse.

Dupuis L., Leon-Del-Rio A., Leclerc D., Company J. M., Herman G., Gibson K.M., Gravel R.A.;

Saudubray J.M., Herman G., Gibson K.M., Gravel R.A.;

"Clustering of mutations in the biotin-binding region of

"Clustering of mutations in the biotin-responsive multiple carboxylase
                                                                                                                                                                                                                                                                                                                                                                                                Genomics [7]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dahmane N., Ait Ghezala G., Gosset P., Chamoun Z.,
Dufresne-Zacharia M.C., Lopes C., Rabatel N., Gassanova-Maugenre
Chettouh Z., Abramowski V., Fayet E., Yaspo M.L., Korn B.,
Blouin J.L., Lehrach H., Poustka A., Antonarakis S.E., Sinet P.M.
Creau N., Delabar J.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Scharfe M., Schoen O., Desario A., Reichelt J., Kauer G., Ramser J., Beck A., Klages S., Hennig S., Riesselmann I., Wehrmeyer S., Borzym K., Gardiner K., Nizetic D., Francis Lehrach H., Reinhardt R., Yaspo M.-L.;
"The DNA sequence of human chromosome 21.";
Nature 405:311-319(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Park H.-S., Toyoda A., Ishii K., Totoki Y., Choi D.-K., Soeda E. Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K., Poli Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D., Reichwald K., Rump A., Schillhabel M., Schudy A., Zimmermann W., Rosenthal A., Kudoh J., Shibuya K., Kawasaki K., Asakawa S., Shintani A., Sasaki T., Nagamine K., Mitsuyama S., Antonarakis Shintani A., Sasaki T., Nordsiek G., Hornischer K., Brandt P., Scharf M., Schoen O., Desario A., Reichelt J., Kauer G., Bloeck Banger T. M., Schoen O., Desario A., Reichelt J., Kauer G., Bloeck
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        spectrum of Hum. Genet.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Minoshima S., Shimizu N., Narısawa n., Mucuur...."
"Structure of human holocarboxylase synthetase gene and mutation of holocarboxylase synthetase deficiency.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shintani A., Asakawa S., Shimizu N., "Genomic sequencing of 1.2-Mb region submitted (NOV-1999) to the EMBL/Gen
                     MEDLINE=98057254;
                                        VARIANTS
                                                                                                                                                                                                       VARIANT HCS ASN-571
                                                                                                                                                                                                                                                                                                                                                                                                                           "Transcriptional map of the 2.5-Mb CBR-ERG involved in down syndrome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 1-92 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hattori M., Fujiyama A., Taylor T.D., Watane Park H.-S., Toyoda A., Ishii K., Totoki Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=98163741;
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PubMed=11735028;
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Taheri S., Christensen E
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                                                                                                                                                                                                                                         mutation and a single base patients.";
Biophys. Acta 1272:168-174
                                      HCS PRO-237 AND MET-550
                                                                                                                                                                                                                                                                                                                                                                                                                48:12-23(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (FEB-1997)
                                                                         Genet.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        holocarboxylase synthetase 109:526-534(2001).
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                                                                         5:1011-1016(1996).
                     PubMed=9396568;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=9503011;
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Y., Eki T., Murakami Y.,
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 Sakamoto
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 Chikaoka H.,
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Y., Saito T.,
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a M.,
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 Takita
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Sinet P.M.,
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F.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   biotin was not elevated in a patient with Pediatr. Res. 42:849-854(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBUNIT: MONOMER.

SUBCELLULAR LOCATION: Cytoplasmic and mitochondrial.

TISSUE SPECIFICITY: MOSTLY EXPRESSED IN MUSCLE, PLACENTA, IN LESSER EXTENT IN THE BRAIN, KIDNEY, PARCREAS, LIVER AND LUNG.

DISEASE: DEFECTS IN HLCS ARE THE CAUSE OF HOLOCARBOXYLASE SYNTHETASE DEFICIENCY (HCS) (OR BIOTIN-RESPONSIVE MULTIPLE CARBOXYLASE DEFICIENCY), AN AUTOSOMAL RECESSIVE DISORDER CHARACTERIZED BY METABOLIC KETOACIDOSIS, HYPERAMMONEMIA, EXCRETION OF ABNORMAL ORGANIC ACID METABOLITES, AND DERMATITIS. CLINICAL AND OF ABNORMAL ORGANIC ACID METABOLITES, AND DERMATITIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COA:carbon-dioxide ligase (ADP-forming)].

CATALYTIC ACTIVITY: ATP + blotin + apo-[3-methylcrotonoyl-COA:carbon-dioxide ligase (ADP-forming)] = AMP + diphosphate + [3-methylcrotonoyl-COA:carbon-dioxide ligase (ADP-forming)].

CATALYTIC ACTIVITY: ATP + blotin + apo-[acetyl-COA:carbon-dioxide ligase (ADP forming)] = AMP + diphosphate + [acetyl-COA:carbon-dioxide ligase (ADP forming)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BIOTIN.
SIMILARITY: WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COA:pyruvate carboxyltransferase].

CATALYTIC ACTIVITY: ATP + biotin + apo-[propanoyl-CoA:carbon-dioxide ligase (ADP-forming)] = AMP + diphosphate + [propanoyl-CoA:carbon-dioxide ligase (ADP-formi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACTTACHMENT OF BIOTIN. ACTS ON VARIOUS CARBOXYLASES SUCH AS ACETYL-COA-CARBOXYLASE, PYRUVATE CARBOXYLASE, PROPIONYL COA CARBOXYLASE, AND 3-METHYLCROTYONYL COA CARBOXYLASE.

CATALYTIC ACTIVITY: ATP + biotin + apo-[methylmalonyl-Coa:pyruvate carboxyltransferase] = AMP + diphosphate + [methylmalonyl-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: POSTTRANSLATIONAL MODIFICATION OF SPECIFIC PROTEIN ATTACHMENT OF BIOTIN. ACTS ON VARIOUS CARBOXYLASES SUCH AS AC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LIGASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   non-profit institutions as long
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EMBL; AP000697; BAA89434.1; JEMBL; AP000703; BAA89434.1; JEMBL; AP000701; BAA89434.1; JEMBL; AP000698; BAA89434.1; JEMBL; AP001698; BAA89550.1; EMBL; AP001726; BAA95551.1; EMBL; AP001726; BAA95511.1; EMBL; AP001726; BAA95510.1; EMBL; AP001864; CAA05056.1; Ligase; SIMILAR MIM; VARIANT TIGRFAMS; InterPro; IPR003142; BPL_C. InterPro; IPR004143; BPL_LipA_LipB InterPro; IPR004408; BirA_ligase. or send an modified and this statement is not removed Pfam; PF03237; BPL_C; 1 Pfam; PF03099; BPL_LipA Genew; EMBL; D23672; entities requires a HGNC:4976; HLCS Multifunctional TIGR00121; birA_ligase; 1. equires a license agreement (See http://www.isb-sib.ch/announce/email to license@isb-sib.ch). 333 BAA1333 BAA04902.1; LipA_LipB; enzyme; Disease mutation JOINED.
JOINED.
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L -> P (IN HCS).
/FTId=VAR_005084.
V -> E (IN HCS; < <10% ACTIVITY) Usage bу in no way

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462

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508

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/FTId=VAR_009197. /FTId=VAR_009196.

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CHS5_USTMA
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Best Local Similarity
Matches 6; Conserv
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Chitin synthase 5 (EC 2.4.1.16) (Chitin-UDP acetyl-glucosaminyl transferase 5) (Class-IV chitin synthase 5).
                                                                                                      Transferase; Glycosyltransferase; Transmembrane; Cell wall; Multigene family.
                                                                                                                                                     InterPro; IPR004835; Fungi_chitin_syn
InterPro; IPR001173; Glycos_transf_2.
Pfam; PF03142; Chitin_synth_2; 1.
                                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ustilago maydis (Smut fungus).
Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;
Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHS5_USTMA
013394;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xoconostle-Cazares B., Ruiz-Herrera J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Umchs5, a gene coding for a class IV chitin synthase in Ustilago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WEDLINE=98123008; PubMed=9454647;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=5270;
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SUBCELLULAR LOCATION: Plasma membrane-bound.
SIMILARITY: BELONGS TO THE CHITIN SYNTHASE FAMILY. SUBFAMILY CLASS
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                                 100.0%;
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/FTId=VAR_009200.

MISSING (IN HCS; 14% OF ACTIVITY).
/FTId=VAR_009201.

E -> K (IN RFF ^.
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V -> M (IN HCS).
/FTId=VAR_009198.
D -> N (IN HCS; ALP
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                              Score 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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855B8E52106D675F CRC64;
                                                                               02A91C8C6B1CBB2D CRC64;
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                              DB 1;
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                              Length 1239;
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                                    Best Local Similarity
Matches 6; Conserv
709 LLLVIA 714
                  1 LLLVIA 6
                                     Conservative
                                  100.08; F1
                                    Pred. No. 6.8e+02;
); Mismatches 0;
                                     Indels
                                     0;
                                     Gaps
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Search completed: January Job time: 6.18182 secs 3, 2003, 15:29:21

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                       Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Perfect score:
                                                                                                                                                                                                                                                                                           Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Searched:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                     l number of hits satisfying chosen parameters:
SPTREMBL_21:*

1: sp_archea:*
2: sp_bacteria:*
3: sp_fung1:*
4: sp_human:*
5: sp_invertebrate
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:
14: sp_unclassific
15: sp_bacteriap:*
16: sp_bacteriap:*
17: sp_archeap:*
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            671580 seqs, 206047115 residues
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sp_plant:*
sp_vrodent:*
sp_vrodent:*
sp_vertebrate:*
sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
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sp_phage:*
                                                                                                                                                                                                       sp_invertebrate:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

16	15	14	13	12	11	10	9	8	7	0	σ	4	ω	2	مبر	Result
24	24	24	24	24	24	24	24	24	24	24	24	24	24	24	24	Score
100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	Query Match I
295	295	281	248	239	232	224	223	193	183	173	159	128	110			Length DB
16	16	16	N	16	17	U	æ	8	10	17	16	G	16	G	13	; B
Q8UAB6	Q8ZDP9	P72696	085820	Q9ZBX3	091СВ9	044086	Q8WET9	Q9MIU4	Q9SIE7	92MT80	09РСВ9	Q9NIQ2	Q8XPU9	Q9NIQ1	Q9DGL8	ID
-	Q8zdp9 yersinia pe	P72696 synechocyst	085820 actinobacil	Q9zbx3 streptomyce	Q9ycb9 aeropyrum p	044086 caenorhabdi	Q8wet9 lyonsia hya	Q9miu4 hyphochytri	Q9sie7 arabidopsis	Q8twz8 methanopyru	Q9pgb9 xylella fas	29niq2 trypanosoma	Q8xpu9 ralstonia s	Q9niq1 trypanosoma	Q9dgl8 gallus gall	Description

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
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713	696	689	672	654	601	509	497	487	469	445	442	427	424	410	392	375	368	361	349	326	317	316	315	311	306	301	297	296
11	2	10	6	16	16	10	16	16	2	16	16	N	16	11	16	16	10	17	10	16	11	ഗ	11	N	2	16	16	4
Q9EPE8	054201	Q8S0A9	Q9BE74	Q9K5Q7	Q930C1	Q40025	Q98M07	067873	Q9JRM9	Q9A164	Q8RGF7	Q9EUU4	Q9AK38	Q923Z0	067832	Q9CD53	Q9SXN7	Q9YBP9	064468	Q9ZCD2	Q8VF60	016463	Q8VG59	Q9F0G9	Q93SG5	Q8UG43	P74131	Q9UG33
Q9epe8 mus musculu	O54201 streptomyce	Q8s0a9 oryza sativ	Q9be74 macaca fasc	Q9k5q7 bacillus ha	Q930c1 rhizobium m	Q40025 hordeum vul	Q98m07 rhizobium l	O67873 aquifex aeo	Q9jrm9 actinobacil	Q9a164 streptococc	Q8rgf7 fusobacteri				067832 aquifex aeo			Q9ybp9 aeropyrum p	O64468 arabidopsis	Q9zcd2 rickettsia	Q8vf60 mus musculu	016463 caenorhabdi	Q8vg59 mus musculu	Q9f0g9 pseudomonas	Q93sg5 corynebacte	Q8ug43 agrobacteri		Q9ug33 homo sapien

ALIGNMENTS

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RESULT 2 Q9NIQ1 ID Q9NIQ1 PRELIMINARY; PRT; 107 AA. AC Q9NIQ1; DT 01-CT-2000 (TrEMBLrel. 15, Created) DT 01-CT-2000 (TrEMBLrel. 15, Last sequence update) DT 01-CT-2000 (TrEMBLrel. 15, Last annotation update)	Best Local Similarity 100.0%; pred. No. 1.8e+02; Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0; 1 LLLVIA 6 9 LLLVIA 14	NCBI_TaxID=9031; [1] SEQUENCE FROM N.A. SEQUENCE FROM N.A. TISSUE=FIBROBLAST; Hartl M., Bister K.; "Suppression of genes in jun-transformed avian fibrobla: "Suppression of genes in jun-transformed avian fibrobla: Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases Submitted (JUL-2000) 1; - SEQUENCE 98 AA; 11564 MW; 30D88E540AADD35B CRC64;	Q9DGLB Q9DGLB pRELIMINARY; PRT; Q9DGLB pr Q9DGLB pr Q9DGLB; pr Q9DGLB; pr Q9DGLB; pr Q9DGLB; pr Q9DGLB; pr Q9DGLB; pr Q1-MAR-2001 (TrEMBLrel. 16, Last sequence update) pr Q1-MAR-2001 (TrEMBLrel. 16, Last annotation update) pr Q1-MA

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EMBL, AL646085; CAD18688.1; -. Plasmid; Complete proteome.
SEQUENCE 110 AA; 12295 MW; 3F8A16A7F019E427 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-20209394; PubMed-10744707; Di Noia J.M., D'Orso I., Sanchez D.O., Frasch A.C.; "AU-rich elements in the 3'-untranslated region of a new mucin-type gene family of trypanosoma cruzi confers mRNA instability and modulates translation efficiency."; J. Biol Chem 275.10210 100201
                                                                                                                                                                                                                                                                                                                             Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S., Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L., Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N., Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
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01-MAR-2002 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
 Mucin-like
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria;
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NCBI_TaxID=5693;
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AF203096; AAF67333.1; -.
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RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Colauto N.B., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
RA Coutinho L.L., Cristofani M., Dias F., Costa M.C.R., Costa-Neto C.M.,
RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Machado M.A., Madeira A.M.B.N., Machado J.A.,
RA Machado M.A., Madeira A.M.B.N., Martins E.M.F., Marsukuma A.Y.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
Nohrear G. M. Nance L.R., Oliveira M.A.
RA Manna A.T., Nohrear F.G., Nunes L.R., Oliveira M.A.
RA Nania A.T., Nohrear G.G., Nunes L.R., Oliveira M.A.
                                          Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
A de Oliveira M.C., de Oliveira R.C., Palimieri D.A., Paris A.,
Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
A Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
A de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
A de Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
A da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
A de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H.,
A Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
A Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
A Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
A Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
A Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
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A Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
A Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
A Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
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A Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
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A Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
A Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
A Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
A Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
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MEDLINE=20209394;
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NCBI_TaxID=5693;
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"AU-rich elements in the 3'-untranslated region of a new mucin-type
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Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D., Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Fajdblyum T.V., Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S., Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M., Venter J.C.;
"Sequence and analysis of Chromosome 2 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q8TWZ8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Slesarev A.I., Mezhevaya K.V., Makarova K.S., Polushin N.N., Shcherbinina O.V., Shakhova V.V., Belova G.I., Aravind L., Natale D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O., Malykh A.G., Koonin E.V., Kozyavkin S.A., "The complete genome of hyperthermophile Methanopyrus kandleri AV19 and monophyly of archaeal methanogens."

Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649(2002).
                                                                                                                                                                                        Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
                                                                                                                                                                                                                                                          09SIE7;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last seq
01-MAR-2002 (TrEMBLrel. 20, Last ann
                                                                                                                                                                                                                                                                                                                 Q9SIE7
                                                                                                                                                                 eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                           STRAIN=CV. COLUMBIA;
MEDLINE=20083487; PubMed=10617197;
                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                   AT2G22170
                                                                                                                                                                                                                                             At2g22170 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE010378; AAM02096.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-AV19 / DSM 6324 / JCM 9639;
MEDLINE=21927647; PubMed=11930014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=2320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Methanopyrus kandleri.
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Similarity 100.0%;
6; Conservative 0
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173 AA;
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                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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2.8e+02;
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on update)
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PNLL...

Q9MIU4;
Q9MIU4;
Q1-CCT-2000 (TrEMBLrel. 15, Created)
Q1-CCT-2000 (TrEMBLrel. 15, Last sequence update)
Q1-CCT-2000 (TrEMBLrel. 21, Last annotation update)
Q1-TUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence up
01-JUN-2002 (TrEMBLrel. 21, Last annotation
                                                                                                                                                                                                           Q8WET9;
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Pfam; PF02790; COX2_TM; 1.
PRINTS; PR01166; CYCOXIDASEII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hudspeth D.S.S., Nadler S.A., Hudspeth M.E.S.;
"A cytochrome c oxidase II molecular phylogeny
peronosporomycetes (Comycetes).";
Mycologia 92:674-684(2000).

EMBL; AF086701; AAF80243.1; -.
InterPro; IPR001505; Copper_CuA.
InterPro; IPR002429; Cyt_C_ox_2.
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                                                              Cytochrome oxidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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NON_TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity nes 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                             65
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193 AA;
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100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 24; DB 8;
Pred. No. 3.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 24;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               D28BD3E4A7A73B67 CRC64;
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                                                                                                                                     sequence update)
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Lyonsia hyalina

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RESULT 10
04408
ID 04408
AC 04408
AC 04408
DT 01-JU
DT 01-JU
DT 01-JU
DT 2K994
GN ZK994
GN Caeno
OC Eukbr
OC Rhabd
OX NCBI
RN [1]
RN [1]
RN SEQUE
RC STRAI
RX MEDLI
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044086;
01-JUN-1998 (TrEMBLrel. 0)
01-JUN-1998 (TrEMBLrel. 0)
01-JUN-2002 (TrEMBLrel. 2)
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Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Jightning J., Lloyd C., McMurray A., Mortinore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

Giribet G., Wheeler W.C.;

Giribet G., wheeler W.C.;
Submitted (SEP-1997) to the
EMBL; AF022977; AABB8611.1;
InterPro; IPR001611; LRR.
InterPro; IPR000483; LRR_Cte
InterPro; IPR000372; LRR_Nte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=BRISTOL N2;
MEDLINE=94150718; PubMed=7906398;
                                                                                                                             Waterston R.;
                                                                                                                                                     STRAIN-BRISTOL N2;
                                                                                                                                                                               SEQUENCE FROM N.A
                                                                                                                                                                                                                                    Submitted
                                                                                                                                                                                                                                                          "The
                                                                                                                                                                                                                                                                                    Davidson S., Wohldmann P.;
                                                                                                                                                                                                                                                                                                            STRAIN-BRISTOL
                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                       Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A
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Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Caenorhabditis elegans
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Similarity 100.0%;
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223 AA;
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LRR_Nterm
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EMBL/GenBank/DDBJ databases.
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                                                                        Q9ZBX3;
Q1-MAY-1999 (TrEMBLrel. 10, C
Q1-MAY-1999 (TrEMBLrel. 21, L
Q1-JUN-2002 (TrEMBLrel. 21, L
Possible integral membrane pr
SCO3959 OR SCD78.26.
                                                                                                                                                                                                                                                                                                                 MEDLINE-99310339; PubMed-10382966;

Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosug
Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K.,
Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
"Complete genome sequence of an aerobic hyper-thermophilic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9YCB9;
01-NOV-1999
01-NOV-1999
01-MAR-2002
                                                                                                                                                                                                                                                                                  EMBL; AP000061; BAA80329.1; -. Hypothetical protein; Complete SEQUENCE 232 AA; 24673 MW;
                                                     Bacteria; Firmicutes;
                                                               Streptomyces coelicolor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Desulfurococcaceae;
NCBI_TaxID=56636;
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STRAIN=A3(2) / M145;
          SEQUENCE FROM N.A
                               NCBI_TaxID=1902;
                                         Actinomycetales;
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                                         Streptomycineae;
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Pred. No. 3.9e+02;
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Pred. No. 3.7e+02;
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                                         Streptomycetaceae;
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                                                     Actinobacteridae;
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RESULT 14
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P72696;
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085820;
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                                                                                                                                                                                                                                                                                                               Winston J.L., Sezate S.A., Dyer D.W., McLaughlin R.E.; "Demonstration of a polyamine requirement for growth of Actinobacillus actinomycetemcomitans, and identification of the putative polyamine transport operon."; Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2).";
Coelicolor A3(2).";
Nature 417:141-147(2002).
EMBL; AL034355; CAA22231.1; -
                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                      Transmembrane;
                                                                                                                                                                                              Pfam; PF00528; BPD_transp; 1.
PROSITE; PS00402; BPD_TRANSP_INN_MEMBR;
                                                                                                                                                                                                                                                                                                                                                                          STRAIN=Y4;
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Bacteria; Proteobacteria;
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01-NOV-1998
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 (TrEMBLrel. 02,
                                                                                                                             Conservative
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AA; 27390 MW;
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Pred. No. 4e+
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Pred. No. 4.1e+02;
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RESULT 15
Q8ZDP9
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Q8ZDP9;
Q8ZDP9;
Q1-MAR-2002 (TrEMBLrel. 20, Cr
Q1-MAR-2002 (TrEMBLrel. 20, Le
Q1-JUN-2002 (TrEMBLrel. 21, Le
                                                                                                                           Query Match
Best Local
                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                              Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G., Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M., Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G., Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V., Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=CO-92 / BIOVAR ORIENTALIS;
MEDLINE=21470413; PubMed=11586360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Sequence analysis of the genome of the unicellular cyanobacterium synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions."; DNA Res. 3:109-136(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synechocystis sp. (strain PCC 6803).
Bacteria; Cyanobacteria; Chroococcales; Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1997 (TrEMBLrel 02, I
01-MAR-2002 (TrEMBLrel 20, I
Hypothetical protein slr0241.
SLR0241
                                                                                                                                                                                                    InterPro; IPR000620; DUF6.
pfam; PF00892; DUF6; 1.
Hypothetical protein; Complete
SEQUENCE 295 AA; 30755 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; D90900; BAA16703.1; -. Hypothetical protein; Complete SEQUENCE 281 AA; 31695 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE=97061201;
                                                                                                                                                                                                                                                                                                                                  "Genome sequence of Yersinia pestis, the causative Nature 413:523-527(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yersinia
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                                                                                                                                                                                                                                                                                                          EMBL; AJ414152; CAC91312.1;
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17
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LLLVIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proteobacteria;
                                                                                                100.0%; ilarity 100.0%; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gamma subdivision; Enterobacteriaceae;
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                                                                                                Score 24; DB 16;
Pred. No. 4.8e+02;
; Mismatches 0;
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08CA1CC1D6D5DA1B
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11747438653C02B7
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                                                                                                   Indels
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Search completed: January 3, 2003, 15:31:59 Job time: 21.3182 secs

Page 6

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Database
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Maximum DB
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                                                      and is
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Listing first 45 summaries
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SUMMARIES
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Compugen Ltd.
                                                score distribution.
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ω 2	32	32	32	32	32	32	32	32	34	Score
94.1	94.1	94.1	94.1	94.1	94.1	94.1	94.1	94.1	100.0	Query Match Length DB
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21	21	21	21	21	21	21	21	22	23	DB
AAG35297	AAG35186	AAG24459	AAG06437	AAG35298	AAG35187	AAG24460	AAG06438	AAE10210	AAU11844	ID
Zea mays protein f	Zea mays protein f	Arabidopsis thalia	Arabidopsis thalia	Zea mays protein f	Zea mays protein f	Arabidopsis thalia	Arabidopsis thalia	Human bone marrow	Peptide ligand for	Description

WPI; 2002-061944/08

Hammond DJ, Wiltshire VR,

Carbonell R,

Shen Щ 05-APR-2000; 2000US-0543188

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TECHNOLOGIES INC.

mutant G p	5	21	433	85.3	29	45
Human G protein-co	AAY90622	21	433	5	29	44
Human G-protein co	AAY03770	20	433	ŗ	29	43
Saccharomyces cere	AAB74887	22	391	ŗ	29	42
	AAY26166	20	391	5	29	41
Cytosolic glycerol	AAW57324	19	391	5	29	40
	AAW60255	19	391	5	29	39
•	AAW30680	19	391	Ģ,	29	38
Drosophila melanog	ABB65431	22	371	Ģ.	29	37
Novel human secret	AAU31812	22	352	ŗ	29	36
Human gene 10 enco	AAB87428	22	261	Ģ	29	35
Human prostate can		22	185	<u>ب</u>	29	34
Human albumin fusi	ABG65354	23	179	<u>ب</u>	29	33
Human gene 10 enco	AAB87351	22	179	.51	29	32
Propionibacterium	AAU65123	22	115	5	29	31
5	AAP60356	7	24	5	29	30
	ABG12286	22	739	8	30	29
	ABG09732	22	739	8	30	28
Novel human diagno	ABG03417	22	739	ω.	30	27
Novel human diagno	ABG21614	22	603		30	26
	AAU77623	23	305	8	30	25
Streptococcus poly	ABP27371	23	305	8	30	24
ţ	AAG17986	21	123	8	30	23
Arabidopsis thalia	AAG17987	21	122	8	30	22
đ	AAU60587	22	98		30	21
CO.	AAG17988	21	74	8	30	20
Human secreted pro	AAY14458	20	70	ω.	30	19
Human ORFX protein	ABP07377	23	52	8	30	18
m	ABB14713	22	51	8	30	
Human secreted pro	AAG03171	21	51	8	30	16
	ABG30281	22	2478	1.	31	15
Novel human diagno	ABG29035	22	2243	1.	31	
ays pro	AAG35185	21	126	4.	32	13
-	ABG60099	23	110	4	32	
Human DITHP polype	ABG60097	23	101		32	11

ALIGNMENTS

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RESULT 1
AAU11844
Prion protein; Prp; ligand; octapeptide motif; scrapie; prion-associated disease; Creutzfeldt-Jakob disease; Gerstmann-Straussler-Scheinker disease; fatal familial insomnia;
                                                                                                                                                                                              feline spongiform encephalopathy; bovine spongiform encephalopathy;
transmissible mink encephalopathy; exotic ungulate encephalopathy;
                                                                                                                                                                                                                                                                                                           AAU11844;
                                                                                                                                                                                                                                                                                                                              AAU11844 standard; peptide; 6 AA
                                                                                               05-APR-2001; 2001WO-US11150
                                                                                                                    18-OCT-2001.
                                                                                                                                         WO200177687-A2.
                                                                                                                                                               Synthetic.
                                                                                                                                                                                     chronic wasting
                                                                                                                                                                                                                                                              Peptide ligand for Prion protein, PrP, #19.
                                                                                                                                                                                                                                                                                     26-MAR-2002
                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                     disease.
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RESULT 2
AAE10210
В
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a ligand of less than 6 kD that binds to a polypeptide containing the sequence GlyTyTGINFOHISGLYGLY (A) or an analogue that is the retro-inverso isomer of (A). The sequence A is an octapeptide motif from the prion protein (PrP). The ligands are identified by binding assays with the peptide (A) or peptides containing (A). The ligands are used for detecting prion proteins (or prions) in biological or environmental samples, e.g. for diagnosis, also for removing them from samples, for treating or retarding development of prion-associated diseases, specially (Treutzfeldt-Jakob diseases (in latrogenic, new variant, familial or sporadic forms), but also cerstmann-Straussler-Scheinker disease, familial insomnia,
              Isolated polynucleotide encoding bone marrow derived polypeptides useful for treating, e.g., Parkinson's, Alzheimer's, cancer, arth Crohn's disease, and inflammatory bowel disease
                                                                                                                                                                                                    07-MAR-2000; 2000US-0519705
19-MAY-2000; 2000US-0574454
14-JUL-2000; 2000US-0616847
30-NOV-2000; 2000US-0250583
                                                                                                                                                                                                                                                                                                                                                                                                       stem cell growth; haematopolesis regulation; immunoregulatory; anaemia; Parkinson's disease; Alzheimer's disease; amyotrophic lateral sclerosis; infection; HIV; malaria; fungal; cancer; autoimmune disorder; arthritis; Crohn's disease; inflammatory bowel disease; leukaemia; gene therapy.
                                                                               WPI; 2001-565565/63.
N-PSDB; AAD17391.
                                                                                                                                          Ford JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   scrapie, bovine or feline spongiform encephalopathy, transmissible mink or exotic ungulate encephalopathy, or chronic wasting disease. The present sequence is a ligand of the invention.
                                                                                                                                                                                                                                                                                  07-MAR-2001; 2001WO-US07274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human
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                                                                                                                                                                         (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                 WO200166558-A1
                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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Pred. No.
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                                 arthritis
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RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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  99US-0130891.
99US-0131449.
99US-0132048.
99US-0132407.
99US-0132484.
99US-0132485.
99US-01324867.
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99US-0130449.
99US-0130510.
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99US-0128234.
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99US-0129845.
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RESULT 4
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Best Loc
Matches
25-FEB-1999
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83.3%;
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1; Mismatches
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XX Protein identification: signal transduction pathway; motabolic pathway; bybridisation assay: genetic mapping; gene expression control; promoter; kt termination sequence; corn. XX XX XX XX XX XX XX XX XX	Query Match 94.1%; Score 32; DB 21; Length 79; Best Local Similarity 83.3%; Pred. No. 1e+02; Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0; Qy 1 IQIWIF 6
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30-AUG-1999;
31-AUG-1999;
01-SEP-1999;
07-SEP-1999;
        Protein identification; signal transduction pathway; metabolic hybridisation assay; genetic mapping; gene expression control;
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        pathway;
promoter;
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          25-FEB 1999
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RESULT 10
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                                                 Protein identification; signal transduction pathway; metabolic hybridisation assay; genetic mapping; gene expression control; termination sequence; corn.
06-SEP-2000
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1.1e+02;
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28-JUN 1999
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28-SEP-1999;
29-SEP-1999;
04-OCT-1999;
05-OCT-1999;
07-OCT-1999;
08-OCT-1999;
                                                                                                                                                                                                                    Human; DITHP; diagnostic and therapeutic polypeptide; bone; testis; skin; cell proliferative disorder; cancer; tumour; autoimmune disorder; brain; inflammatory disorder; viral infection; bacterial infection; seizure; fungal infection; parasitic infections; developmental disorder; breast; endocrine disorder; metabolic disorder; neurological disorder; cervix; gastrointestinal disorder; transport disorder; gene therapy; kidney;
29-AUG-2001; 2001WO-US27127.
                                              14-MAR-2002
                                                                                   WO200220754-A2
                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                 Human DITHP polypeptide #155
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5; Conserv
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9908-0161392

9908-0161992
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990S-0159294.
990S-0159295.
990S-0159329.
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99US-0158029.
99US-0158232.
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99US-0156458.
99US-0156596.
99US-0157117.
                                                                                                                                                                                             bone marrow; lung; ovary; pancreas; prostate; spleen;
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83.3%;
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1.1e+02;
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RESULT 12
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CC polynucleotides and their associated polypeptides (DITHP polypeptides).
CC The sequences of the invention are used in the treatment and diagnosis of CC cell proliferative disorders (e.g. atherosclerosis, cirrhosis), cancers
CC cervix, kidney, lung, ovary, pancreas, prostate, skin, spleen, testis or CC thymus), autoimmune/inflammatory disorders (e.g. asthma, broachitis, psoriasis, osteoporosis), viral infections, bacterial infections, fungal infections, parasitic infections, developmental disorders (e.g. anaemia, cepilepsy), seizure disorders (e.g. cerebral palsy, spina bifida), CC endocrine disorders (e.g. thrombosis, aneurysm), metabolic disorders (e.g. obesity, diabetes), neurological disorders (e.g. stroke, amyotrophic lateral sclerosis, multiple sclerosis), gastrointestinal CC amyotropic dystrophy, catatonia, peripheral neuropathy). Sequences (e.g. myotonic dystrophy, catatonia, peripheral neuropathy). Sequences CC (e.g. myotonic dystrophy, catatonia, peripheral neuropathy).
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05-SEP-2000

06-SEP-2000

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Gerstin E
Marwaha R
                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 An isolated polynucleotide useful in diagnostics and therapeutics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (INCY-) INCYTE GENOMICS INC.
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                                                                                     1 IQIWIF 6
                                                                     IQIWLF
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DB; ABK71688.
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EH,
a R, (
                                                                                                                                       Similarity
5; Conserv
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2000US-229749P.
2000US-229750P.
2000US-229750P.
2000US-230514P.
2000US-230514P.
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2000US-230597P.
2000US-230599P.
                                                                                                                                        Conservative
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u JY, Wright RJ, Gietzen D, Liu TF, Yap PE, Dah

Bradley DL, Rohatgi SD, Harris B, Roseberry AM;

Peralta CH, David MH, Panzer SR, Flores V, Daff

Chen AJ, Chang SC, Au AP, Inman RR;
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                                                                                                                                                       94.1%;
83.3%;
                                                                                                                                     Score 32; DB
Pred. No. 1.3e
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1.3e+02;
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ABG60099 standard; Protein;

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07-SEP-2000
                 The invention relates to human diagnostic and therapeutic (dithp) polynucleotides and their associated polypeptides (DITHP polypeptides). The sequences of the invention are used in the treatment and diagnosis of cell proliferative disorders (e.g. atherosclerosis, cirrbosis), cancers (e.g. tumours of the adrenal gland, bone, bone marrow, brain, breast, cervix, kidney, lung, ovary, pancreas, prostate, skin, spleen, testis or thymus), autoimmune/inflammatory disorders (e.g. asthma, bronchitis, psoriasis, osteoporosis), viral infections, bacterial infections, fungal infections, parasitic infections, developmental disorders (e.g. anaemia, epilepsy), seizure disorders (e.g. cerebral palsy, spina bifida), endocrine disorders (e.g. thrombosis, aneurysm), metabolic disorders (e.g. obesity, diabetes), neurological disorders (e.g. stroke, amyotrophic lateral sclerosis, multiple sclerosis), gastrointestinal disorders (e.g. stroke, amyotrophic lateral sclerosis, multiple sclerosis), gastrointestinal
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Gerstin E
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                                                                                                                                                                                                                                                                                                                                                                                                              Claim 29; Page 622; 686pp; English.
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disorders (e.g. ulcerative colitis,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human DITHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        isolated polynucleotide useful in diagnostics and therapeutics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EH, Peralta
R, Chen AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABK71690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lincoln SE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yu JY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US - 230518P
2000US - 230519P
2000US - 230595P
2000US - 230599P
2000US - 230599P
2000US - 230599P
2000US - 230610P
2000US - 230610P
2000US - 230865P
2000US - 230981P
2000US - 231163P
2000US - 231167P
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2000US-230505P
2000US-230514P
2000US-230515P
2000US-230517P
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Peralta CH, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Altus CM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RJ, Gietzen D, Liu ...
RJ, Gietzen D, Liu ...
Rohatgi SD, Harris B, Rose...
Pavid MH, Panzer SR, Flores V, and transport disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Roseberry AM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hillman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dahl CR;
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δÃ
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RESULT 13
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20-MAY-1999;
21-MAY-1999;
24-MAY-1999;
25-MAY-1999;
27-MAY-1999;
01-JUN-1999;
03-JUN-1999;
                                                                                                                                                                                                                                                                                  28-APR-1999;
30-APR-1999;
30-APR-1999;
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05-MAY-1999;
06-MAY-1999;
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25-MAR-1999;
29-MAR-1999;
01-APR-1999;
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14-MAY-1999;
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14-MAY-1999;
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07-MAY-1999
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21-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (e.g. myotonic dystrophy, catatonia, peripheral neuropathy). Sequence: ABG59943-ABG60220 represent human DITHP polypeptides of the invention
                                                                                                                                                                                                                                                                                                                                                                                 16-APR-1999,
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                                                                                                               3-MAY-1999;
3-MAY-1999;
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|QIWLF 62
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99US-0128714.
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Pred. No.
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ches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pathway;
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04-JUN 1999
08-JUN 1999
110-JUN  9908-0137502
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Best Local Similarity
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29-SEP-1999
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                                  99US-0147303
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99US-01474793
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99US-0149902
99US-0150864
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99US-0150866
99US-0151080
99US-0150818
99US-0160815
99US-0161100
99US-0161100
99US-01611159
99US-01611159
99US-01611159
99US-01611159
 94
83
Score 32;
Pred. No.
DB 21;
1.6e+02;
           Length 126;
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Matches

Conservative

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Mismatches

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ABG29035

ABG29035;

18-FEB-2002

RESULT 14

K K X B X D X A X

WO200175067-A2

Homo sapiens

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CC for identifying expressed genes. (I) is useful in gene therapy techniques (II) (II) is useful for generating antibodies against it, detecting or cyling (II) is useful for generating antibodies against it, detecting or cyling a polypeptide in tissue, as molecular weight markers and as CC among the supplement. (II) and its binding partners are useful in medical cyling of sites expressing (II). (I) and (II) are useful for treating CC disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations. CC responsible for genetic disorders or other traits to assess biodiversity amino acid sequences of data and products dependent on DNA and CC amino acid sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed consecution, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 20; SEQ ID No 59394; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-MAR-2000; 2000US-0540217
23-AUG-2000; 2000US-0649167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; chromosome mapping; gene mapping; gene therapy; forension food supplement; medical imaging; diagnostic; genetic disorder
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                                                                                                                                                                   at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    polypeptide (II) sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel human diagnostic protein #29026.
                             Conservative
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                                                91.2%;
83.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  olated polynucleotide (I) and (I) is useful as hybridisation probes,
                             1;
                                                Score 31;
Pred. No.
                             Mismatches
                                                4.2e+03;
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                          0;
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                                                                    Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                              (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in reating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mappping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutatio responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 20; SEQ ID No 60640; 103pp; English
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23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                             at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel human diagnostic protein #30272
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1 IQIWIF 6
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                                                                                          91.2%;
83.3%;
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                                                                                          Score 31;
Pred. No.
                                                                      Mismatches
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                                                                                          4.6e+03;
                                                                                                                  DB
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                                                                                                              Length 2478;
                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mutations
                                                                      0,:
                                                                    Gaps
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Drmanac RT, Liu C,

(HYSE-) HYSEQ INC

N-PSDB; AAS93222.

WPI; 2001-639362/73

Query Match
Best Local Similarity
Matches 5; Conserv

0;

Sequence

2243 AA

Search completed: January 3, 2003, 15:28:40 Job time : 28.5909 secs В

563 IQIWMF 568

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Title:
Perfect score:
Sequence:
                Scoring table:
                                                                                                                                                                                                 OM protein - protein search, using sw model
                                                                                                                                                                   Run on:
BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                         January 3, 2003, 15:25:00; Search time 9.95455 Seconds (without alignments) 57.944 Million cell updates/sec
                                                      US-09-543-188A-21
34
1 IQIWIF 6
                                                                                                                                                                                                                                                       GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.
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Minimum DB seq length: 0
Maximum DB seq length: 2000000000

al number of hits satisfying chosen parameters:

283224

283224 seqs, 96134422 residues

earched:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	5	4	ω	2	щ	NO.	Result
29	29	29	29	29	29	29	29	29	29	29	29	29	29	30	30	30	30	30	30	30	30	31	32	32	32	33	33	33	Score	
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hypothetical prote	hypothetical prote	ribosomal protein	SecY-independent t	30S ribosomal prot	7	6	ribosomal protein	1	pro	aquaporin Z, water	aquaporin [importe	al pro	thetical p	te-spe	o cell	0	ribosomal protein	glutaredoxin-like	ribosomal protein	ribosomal protein	\vdash	probable polysacch	NADH2 dehydrogenas			a	cal pr	rotei	Description	

4.4	43	42	41	40	39	38	37	36	35 5	34	ω ω	32	31	30
28	28	28	28	28	28	28	28	28	29	29	29	29	29	29
82.4	82.4	82.4	82.4	82.4	82.4	82.4	82.4	82.4	85.3	85.3	85.3	85.3	85.3	85.3
228	227	219	205	122	122	92	90	71	978	920	720	583	391	373
N V	N	1	N	N	N	N	2	2	<u> </u>	μ	N	N	N	2
G83115	T11185	R3KT3	PC2191	AC1808	A31090	A32127	T27041	T51537	RGBYI3	PXNCP	T02361	T02382	S40059	PW0042
are synthase to ch 30S ribosomal prot	H+-transporting tw	ribosomal protein		ATP synthase chain	hypothetical 14K p	small nuclear ribo	hypothetical prote	hypothetical prote	regulatory protein	H+-exporting ATPas	hypothetical prote	hypothetical prote	glycerol-3-phospha	activin - fruit fl

ALIGNMENTS

Query Match 97.1%; Score 33; DB 2; Length 285; Best Local Similarity 83.3%; Pred. No. 47;	A;Reference number: 219842 A;Reference number: 219842 A;Reference number: 219842 A;Reference number: 219842 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-285 <will> A;Cross-references: EMBL:Z81109; PIDN:CAB03254.1; GSPDB:GN00023; CESP:R10D12.11 A;Experimental source: clone R10D12 C;Genetics: A;Gene: CESP:R10D12.11 A;Map position: 5 A;Introns: 51/2; 165/3; 240/3 C;Superfamily: Caenorhabditis hypothetical protein C49G7.2</will>	2.11 - Caenorhabdi elegans nce_revision 15-0c	Query Match 97.1%; Score 33; DB 2; Length 282; Best Local Similarity 83.3%; Pred. No. 47; Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0; Qy 1 IQIWIF 6 [: Db 275 IQVWIF 280	A;Status: preliminary A;Molecule type: DNA A;Residues: 1-282 <arn> A;Cross-references: GB:D89861; NID:g4115781; PIDN:BAA36537.1; PID:d1037523; PID:g4115 C;Genetics: A;Genem: rps3 A;Genome: mitochondrion C;Keywords: mitochondrion</arn>	R;Ohta, N.; Sato, N.; Kuroiwa, T. Nucleic Acids Res. 26, 5190-5198, 1998 A;Title: Structure and organization of the mitochondrial genome of the unicellular re A;Reference number: A58930; MUID:99030526; PMID:9801318 A;Accession: C58933	RESULT 1 C58933 C58933 C589634 C589645: mitochondrion Cyanidioschyzon merolae mitochondrion C;Species: mitochondrion Cyanidioschyzon merolae C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 05-Nov-1999
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probable small nuclear ribonucleoprotein E [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana A;Reference number: A85001; MUID:20083488; PMID:10617198 A;Accession: F85354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           K:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: G83831
                  R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon,
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R; anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Nature 402, 769-777, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             small nuclear ribonucleoprotein homolog [imported] - Arabidopsis thaliana
C;Speckes: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001
C;Accession: F85354
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                                                                          C; Accession: A84568
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C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
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     Nature 402,
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sidues: 1-360 <STO>
coss-references: GB:AP001512; GB:BA000004; NID:g10174030; PIDN:BAB05174.1;
Experimental source: strain C-125
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Residues: 1-86 <STO>
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83.3%;
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59;
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                                    C.Y.;
lon, L.
                                                                                                                                            A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-394 <PAR>
                                                     A; Gene: Cj1413
C; Superfamily:
                                                                                                          A;Cross-references: GB:AL139078;
A;Experimental source: serotype
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                                                                          Cj1413c
                                                       kpsD protein
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R;Beaton, M.J.; Roger, A.J.; Cavalier-Smith, T.
J. Mol. Evol. 47, 697-708, 1998
A;Title: Sequence analysis of the mitochondrial genome (A;Reference number: Z17505; MUID:99065763; PMID:9847412
A;Accession: T12401
                                                                                                                                            probable polysaccharide modification protein Cj1413c [imported] - Campyloba
C;Species: Campylobacter jejuni
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Note: ND4
C; Superfamily: NADH dehydrogenase (ubiquinone) chain 4
C; Keywords: membrane-associated complex; mitochondrion;
A;Title: The genome sequence A;Reference number: A81250; MA;Accession: E81286
                                                           C;Accession: E81286
R;Parkhill, J.; Wern, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C. C.W.; Quall, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Nature 403, 665-668, 2000
                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
"hes 5; Conserv?
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A; Residues: 1-495 <BEA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-88 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Genome: mitochondrion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:AF064823; NID:g4091912; PID:g4091917;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Status: preliminary; translated
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83.3%;
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                 of the food-borne pathogen Campylobacter jejuni MUID:20150912; PMID:10688204
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Pred. No.
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Pred. No. 1
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23;
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91.2%;

Score Pred.

No.

DB 2; 1.6e+02;

Length

GB:AL111168; NID:96968723; PIDN:CAB73837.1; O2, strain NCTC 11168

PID: 9696

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R;Tanaka, M.; Wakasugi, T.; Sugita, M.; Shinozaki, K.; Sugiura, M.
Proc. Natl. Acad. Sci. U.S.A. 83, 6030-6034, 1986
A;Title: Genes for the eight ribosomal proteins are clustered on the chloroplast genome A;Reference number: A94118; MUID:86287388; PMID:3016736
A;Recession: E25943
A;Residues: 1-218 <TAN>
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tibosomal protein S3, chloroplast - spinach chloroplast C;Species: chloroplast Spinacia oleracea (spinach) C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 22-Jun-1999 C;Accession: S01978 R;Zhou, D.X.; Quigley, F; Massenet, O.; Mache, R. Mol. Genet. 216, 439-445, 1989 A;Title: Cotranscription of the S10- and spc-like operons in spinach chloro A;Reference number: S01976; MUID:89313684; PMID:2747623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: The compact. A38013
A;Reference number: A38013
A;Reference number: gene organization, sites, features
A;Contents: annotation; gene organization, sites, features
A;Contents: annotation; gene organization, sites, features
A;Reference number: A38013
A;Refere
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C;Superfamily: Escherichia coli ribosomal protein
C;Keywords: chloroplast; protein biosynthesis; rik
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                                                                                                                                                                                                                              A;Genome: chloroplast C;Superfamily: Escherichia coli ribosomal protein
                                                                                                                                                                                                                                                                                                                                                                                                           A;Accession: S01978
A;Molecule type: DNA
A;Residues: 1-218 <ZHO>
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Shinozaki, K.; Ohme, M.; Tanaka, M.; Wakasugi, T.; Hayashida, N.; Watsubaya
eno, H.; Kanogashira, T.; Yamada, K.; Kusuda, J.; Takaiwa, F.; Kato, A.; Toh
EMBO J. 5, 2043-2049, 1986
EMBO J. 5, 2043-2049, 1986
EMBO J. 5, 2043-2049, 1986
                                                                                                                                                                                                                                                                                                                                        C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:X13336; NID:g12307; PIDN:CAA31715.1;
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A; Residues: 1-218 <SUG>
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Keywords: chloroplast;
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Kato, A.; Tohdoh,
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ribosomal protein S3, mitochondrial - red alga (Chondrus crispus) mitochondrion c;Species: mitochondrion Chondrus crispus (carragheen) C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 21-Jul-2000 C;Accession: S59085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Reference number: A70300; MUID:98196666; PMID:9537320 A;Accession: E70340
R;Leblanc, C.; Boyen, C.; Richard, O.; Bonnard, G.; Grienenberger, J.M.; Kloareg, J. Mol. Biol. 250, 484-495, 1995
A;Title: Complete sequence of the mitochondrial DNA of the rhodophyte Chondrus cr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            glutaredoxin-like protein - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 05-Nov-1999
C;Accession: E70340
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                                                                                                                                               S59085
                                                                                                                                                                  RESULT
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J. Mol. Evol. 3
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| 138 | IEIWVF | 143
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  mitochondrial DNA of the rhodophyte Chondrus crispu
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to the EMBL Data
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #text_change 13-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 220;
                                                                                                                                                                                                                                                                                                                                                  Length 229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      PID:g2983104; GB:AE00
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A; Gene: CES
A; Introns:
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                                                                                                                                                                                                                                                      related to cell protein precursor [imported] - Neurospora crassa N;Alternate names: protein B24P7.180 C;Species: Neurospora crassa C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change C;Accession: T50963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Watches 5; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 submitted to the EMBL Data Library, November 1995 A;Description: The sequence of C. elegans cosmid C02F12. A;Reference number: Z21473
A; Map
                 C;Genetics:
A;Gene: NCSP:B24P7.180
                                                            A; Experimental source: BAC
                                                                                                       A; Molecule type: DNA
A; Residues: 1-347 <SCH>
                                                                                                                                             A; Status: preliminary
                                                                                                                                                                      A; Reference number: Z25286
A; Accession: T50963
                                                                                                                                                                                                                R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; submitted to the Protein Sequence Database, July 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-309 <MIL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-240 <LEB>
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A;Accession: S59085
A;Status: nucleic acid sequence not shown; translation
                                                                                   A;Cross-references:
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;Gene: CESP:C02F12.1
·***rons: 23/3; 58/3; 83/3; 140/3; 178/3; 257/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cross-references: EMBL:U41545; PIDN:AAA83189.1; CESP:C02F12.1
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A;Experimental source: strain NCTC 3438
C;Superfamily: Haemophilus paragallinarum type II site-specific deoxyribonuclease
                                                                                                                                                                                                                                                                             A;Status: preliminary; not compared with conceptual translation A;Molecule type: DNA A;Residues: 1-488 <SUG>
                                                                                                                                                                                                                                                                                                                              Bull. Inst. Chem. Res. Kyoto Univ. 71, 338-342, 1993
A;Title: Nucleotide sequence of the gene of HgaI restriction endonuclease.
A;Reference number: A59239
A;Accession: C59240
                                                                                                                                                                                                                                                                                                                                                                                                                    type II site-specific deoxyribonuclease (EC 3.1.21.4) HgaI - Haemophilus paragallinar
C;Species: Haemophilus paragallinarum
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 20-Jun-2000
C;Accession: C59240
Search completed: January Job time: 10.9545 secs
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ATPZ_ANASP
                                                                                       GPD1_YEAST
GP22_HUMAN
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YL11_CAEEL
T2G1_HAEGA
Y052_BUCAI
                    RS3_BUCAK
RR3_GUITH
RR3_CYAPA
RS3_ECOLI
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						P73594 synechocyst		049195 arabidopsis			024695 synechococc

ALIGNMENTS

RESULT 1

MTGA_ACICA

STANDARD;

PRT;

224 A

024849; 15-DEC-1998 (Rel. 3 15-DEC-1998 (Rel. 3 16-OCT-2001 (Rel. 4

Acinetobacter Bacteria;

NCBI_TaxID=471;

Acinetobacter calcoaceticus.

Proteobacteria; gamma subdivision; Moraxellaceae;

MTGA.

15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Monofunctional biosynthetic peptidoglycan transglycosylase
(EC 2.4.2.-) (Monofunctional TGase).

37, Created)
37, Last sequence 40, Last annotation

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Query Match
Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=BD413 / ADP1;
MEDLINE=95400495, PubMed=7670642;
Geissdoerfer W., Frosch C.S., Haspel G., Ehrt S., Hillen W.;
"Two genes encoding proteins with similarities to rubredoxin rubredoxin reductase are required for conversion of dodecane lauric acid in Acinetobacter calcoaceticus ADP1.";
                                                                                                              Pfam; PF00912; Transglycosyl; 1. ProDom; PD001895; GT_51; 1.
                                                                                                                                                                                                                                                                                                                                     -!- FUNCTION: CELL WALL FORMATION (BY SIMILARITY).
-!- PATHWAY: FINAL STAGES IN PEPTIDOGLYCAN SYNTHESIS (BY
-!- SUBCELLULAR LOCATION: Membrane-associated (Potential)
-!- SIMILARITY: TO THE N-TERMINAL OF BACTERIAL CLASS IA
                                                                              Peptidoglycan synthesis; Cell wall; Transferase; Transmembrane. TRANSMEM 8 30 POTENTIAL.
                                                                                                                                                            EMBL; Z46863; CAA86932.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-BD413 / ADP1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Microbiology 141:1425-1432(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A
                                                                                                                                              InterPro;
                                                                                                                                                                                                                                                                                                                           BINDING PROTEINS.
                                                                                                                                              IPR001264; GT_51.
                                                               224 AA;
               94.1%;
                                                               26712 MW;
; Score 32; DB; Pred. No. 26; 1; Mismatches
                                                                 F1E5F114FC14E2FE CRC64;
                                 <u>.</u>
                                 Length 224;
                                                                                                                                                                                                                                                                                                                                                                                                                                        superoxide
                                                                                                                                                                                                                                                                                                                                                                        (BY SIMILARITY).
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RR3_AR
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Best Local
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                                                                                                                                                                                                                                                                                                                                  EMBL; AP000423; BAA84423.1; ...
Interpro; IPR004044; KH_TYPE_2.
Interpro; IPR0010351; Ribosomal_S.
Pfam; PF00189; Ribosomal_S.C; 1.
Pfam; PF00417; Ribosomal_S.N; 1.
TICRFAMS; TIGR01009; IPSC_bact; 1.
PROSITE; PS00823; KH_TYPE_2; 1.
PROSITE; PS00548; RIBOSOMAL_S.3; 1.
                                                                                                                                          TOIdS
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                                                                                      RR3_SPIOL
P09595;
01-MAR-1989
01-MAR-1989
                                                                                                                                                                                                                                                                                                               Ribosomal
DOMAIN
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                                                           Chloroplast
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sato
         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                        Chloroplast
                                   Spinacia oleracea
                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=cv. Columbi
MEDLINE=20039611;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Spermatophyta; eurosids II; B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chloroplast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-MAY-2000
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                                                                           L5-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Complete structure of the chloroplast genome
                                                                                                                                                                                             209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Res. 6:283-290(1999).
SIMILARITY: BELONGS TO THE S3P FAMILY OF RIBOSOMAL PROTEINS SIMILARITY: CONTAINS 1 KH TYPE-2 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S., Nakamura Y., Kaneko T., A
                                                                                                                                                                                                                      IQIWIF 6
                                                                                                                                                                                             IKIWIF 214
                                                                                                                                                                                                                                              5; Conserv
                                                                                                                                                                                                                                                                                                                protein;
47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Viridiplantae;
                                                                                                                                                                                                                                                                                                   218 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Columbia;
                                                        (Rel. 10, Created)
(Rel. 10, Last sequenc)
(Rel. 41, Last annotat)
30S ribosomal protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Rel. 39, Created)
(Rel. 39, Last sequence u.)
(Rel. 40, Last annotation
30S ribosomal protein S3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Magnoliophyta;
                                                                                                                             STANDARD;
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                                 (Spinach).
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                                                                                                                                                                                                                                                                                                 25188 MW;
                                                                                                                                                                                                                                                          88.2%;
83.3%;
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                                                                                                                                                                                                                                              1;
                                                                                                                                                                                                                                                                                                               KH TYPE-2.
                                                                                                                                                                                                                                                             Pred. No.
                                                                                                                                                                                                                                                                        Score 30;
                                                                                                                             PRT;
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                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                 763CB03F46D74888 CRC64;
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of Arabidopsis
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                                                                                                                                                                                                                                                                        Length 218;
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RR3_TOBAC
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RR3 TOBAC SILL.

P06357;

r 01-JAN-1988 (Rel. 06, Created)

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DT 15-JUN-2002 (Rel. 41, Last annotation

15-JUN-2003 (Rel. 41, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
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InterPro; IPRO01351; Ribosomal_S3.
Pfam; PF00189; Ribosomal_S3_C; 1.
Pfam; PF00417; Ribosomal_S3_N; 1.
TIGRPAMS; TIGRO1009; TPSC_bact; 1.
PROSITE; PS50832; KH_TYPE_2; 1.
PROSITE; PS00548; RIBOSOMAL_S3; 1.
                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=89313684; PubMed=2747623;
Zhou D.X., Quigley F., Massenet O., Mache R.;
"Cottranscription of the S10- and spc-like operons
chloroplasts and identification of three of their
Mol. Gen. Genet. 216:439-445(1989).
STRAIN=cv. Bright Yellow Shinozaki K., Ohme M., Ta
                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                    Chloroplast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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PIR; S01978; R3SP3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       between the Swiss Institute of Bioinf
the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
                                                                                                                  NCBI_TaxID=4097;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ribosomal protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X13336; CAA31715.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IKIWIF 214
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5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      218 AA;
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83.3%;
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   Tanaka
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                                 4.
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Wakasugi T.,
                                                                                                                                                                                                                                                                                                                         S3.
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60;
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   Hayashida
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InterPro; IPRO01351; Ribosomal_S3.
Pfam; PF00189; Ribosomal_S3_C; 1.
Pfam; PF00417; Ribosomal_S3_N; 1.
TIGRPAMS; TIGRO1009; TPSC_bact; 1.
PROSITE; PS50823; KH_TYPE_2; 1.
PROSITE; PS50823; KH_DOSOMAL_S3; 1.
                               RR3_EPIVI
P30055;
01-APR-1993
01-APR-1993
15-JUN-2002
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Tanaka M., Wakasugi T., Sugita M., Shinozaki K., Sugitra M.;
Tanaka M., Wakasugi T., Sugita M., Shinozaki K., Sugitra M.;
Tanaka M., Wakasugi T., Sugita M.;
Tanaka M., Sugita M.;
Tanaka M., Sugita M.;
Tanaka M., Sugita M.;
Tanaka M.;
T
                                                                                                                                                                                                                           Spermatophyta; Magnoliophyta; Rsteridae; euasterids I; Lamia NCBI_TaxID=4177;
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SEQUENCE FROM N.A. MEDLINE=93021155; PubMed=1404416;
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"The complete nucleotide sequence of the tobacco chloroplast genome:
                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae;
                                                                                                                                                                                                                                                                                                                        Chloroplast.
                                                                                                                                                                                                                                                                                                                                              Epifagus virginiana
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(Rel. 25, Last sequence update)
(Rel. 41, Last annotation update)
30S ribosomal protein S3.
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83.3%;
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                                                                                                                                                                                                                                                                                            Streptophyta;
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                                                                 This SWISS-PROT entry is copyright. It is produced through a cobetween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                               J. MOL. Biol. 250:484-495(1995).
-!- SUBCELLULAR LOCATION: Mitochondrial.
-!- SIMILARITY: BELONGS TO THE S3P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RPS3
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PROSITE; PS50823; KH_TYPE_2; FALSE_NEG
PROSITE; PS00548; RIBOSOMAL_S3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001351; Ribosomal_S3. Pfam; PF00189; Ribosomal_S3_C; 1. Pfam; PF00417; Ribosomal_S3_N; 1.
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J. Mol. Evol. 35:304-317(1992).
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01-FEB-1996
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                          EMBL; Z47547; CAA87601.1;
                                                                                                                                                                                                                                                                                                                            organization."
                                                                                                                                                                                                                                                                                                                                               Chondrus crispus (Gigartinales).
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                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=95341681;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota;
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  InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                     C., Boyen
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                                                                                                                                                                                                                                                                                                                                                                                                                     PubMed=7616569;
C., Richard O.,
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Pfam; PF000355; transmembrane4; 1.

PROSITE; PS00421; TM4_1; FALSE_NEG.

Hypothetical protein; Transmembrane.
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      01-NOV-1995 (Rel. 32, Created)
                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rhabditidae; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; NCBI_TaxID=6239;
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Ol-NOV-1997 (Rel. 35, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Hypothetical protein CO2F12.1 in chromosome x
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Pfam;
                                                                                                                                                                                                                                                                                                 EMBL; U41545; AAK39137.1; -WormPep; C02F12.1; CE25749.
                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a continuous the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is
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                                                                                                                                                                                                  SEQUENCE
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                                                                                               238 QIWIF 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                      mitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
SUBCELLULAR LOCATION: Integral membrane protein (Potential).
SIMILARITY: SOME, TO THE TETRASPANIN (TM4SF) FAMILY.
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PF00417;
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277 AA;
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Ribosomal_S3_N; 1.
                                 STANDARD;
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Pred. No.
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Pred. No.
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POTENTIAL.
; 8084221CBD4C541D CRC64;
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76;
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RESULT 9
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Best Local
use by non-profit institutions as long a modified and this statement is not removed. entitles requires a license agreement (See lor send an email to license@isb-sib.ch).
                                                        This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restr
                                                                                                               MEDLINE=20445173; PubMed=10993077; Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.; Senome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. APS.";
Nature 407:81-86(2000).
-!- SIMILARITY: STRONG, TO E.COLI YIBN AND H.INFLUENZAE HI0744.
                                                                                                                                                                                                                                                                                                                                                                                             Y052_BUCAI
P57160;
                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN-Tokyo 1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a copyright the EMBL between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and formatical statement is not removed.
                                                                                                                                                                                                                                                                     symbiotic bacterium).
Bacteria; Proteobacteria; gamma subdivision; Buchnera
                                                                                                                                                                                                                                                                                      symbiotic
                                                                                                                                                                                                                                                                                                       Buchnera aphidicola
                                                                                                                                                                                                                                                                                                                                              16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; D17388; BAA04208.1; -. REBASE; 1096; HgaI.
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16-OCT-2001 (Rel.
                                                                                                                                                                                                                                                          NCBI_TaxID=118099;
                                                                                                                                                                                                                                                                                                                                   Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
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Bull. Inst. Chem. Res., Kyoto Univ. 71:338-342(1993).
-i- FUNCTION: RECOGNIZES THE DOUBLE-STRANDED SEQUENCES GACGC AND GCG-
AND CLEAVES RESPECTIVELY 10 BASES AFTER G-1 AND 10 BASES BEFORE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sugisaki H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-NCTC 3438;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 5; Conserv
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40, Last annotation update)
on enzyme HgAI (EC 3.1.21.4)
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               http://www.isb-sib.ch/announce,
                            Usage
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16-OCT-2001 (Rel. 40, Last sequence I

16-OCT-2001 (Rel. 40, Last sequence I

15-JUN-2002 (Rel. 41, Last annotation up

Incomplast 30% ribosomal protein S3.
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Matches 4
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Best Local S
Matches 5
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Pfam; PF00199; Ribosomal_S3_C; 1.

Pfam; PF00417; Ribosomal_S3_N; 1.

SMART; SM00322; KH; 1.

TIGRFAMS; TIGR01009; TPSC_bact; 1.

PROSITE; PS00548; RIBOSOMAL S3: 1
                                                                                                                                                                                                                                                                                                                                                                                   Lemieux C., Otis C., Turmel M.;

"Ancestral chloroplast genome in Mesostigma viride revebranch of green plant evolution.";

Nature 403:649-652(2000).

-!- SIMILARITY: BELONGS TO THE S3P FAMILY OF RIBOSOMAL
-!- SIMILARITY: CONTAINS 1 KH TYPE-2 DOMAIN.
                                                                                                                                                                                                                       EMBL; AF166114; AAF43809.1; -.
InterPro; IPR004044; KH_TYPE_2.
InterPro; IPR004087; KH_dom.
InterPro; IPR001351; Ribosomal_S3.
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Eukaryota; Viridiplantae; Streptophyta; Mesostigmatophyceae; Mesostigmatales; Mesostigmataceae; Mesostigma.
                                                                                                                      Ribosomal protein;
                                                                                                                                                                                                                                                                                     entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute. There are no restrictions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein; Complete proteome. SEQUENCE 144 AA; 16921 MW; 87D669CDAD999ECB CRC64;
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PS00548; RIBOSOMAL_S3; 1.
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P06356;
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Pfam; PF00189; Ribosomal_S3_N; 1.
Pfam; PF00417; Ribosomal_S3_N; 1.
TIGRRAMS; TIGR01009; rpsC_bact; 1.
PROSITE; PS50823; KH_TYPE_2; 1.
PROSITE; PS00548; RIBOSOMAL_S3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Structure and organization of Marchantia polymorpha chloroplast genome. III. Gene organization of the large single copy region from rbcL to trnI(CAU).";
J. Mol. Biol. 203:333-351(1988).
                                                                                                                                                                                                                                                                                                                                                                                                        Ribosomal protein;
DOMAIN 46
SEQUENCE 217 AA;
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Nature 322:572-574(1986).
-!- SIMILARITY: BELONGS TO THE S3P FAMILY OF
-!- SIMILARITY: CONTAINS 1 KH TYPE-2 DOMAIN.
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Ozeki H.;
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MEDLINE=89068687; PubMed=3199436;
Fukuzawa H., Kohchi T., Sano T., Shirai H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Marchantiopsida; Marchantii
Marchantiaceae; Marchantia.
NCBI_TaxID=3197;
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InterPro; IPR001351; Ribosomal_
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, Shiki Y., Ta
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                                                                                                STANDARD;
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Takeuchi M.,
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Pred. No.
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Chang Z., A
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92;
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Inokuchi H.,
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Best Local
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                                                                                              Chlorella vulgaris.
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P56365;
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Chlorellaceae; Chlorella.
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15-JUL-1998 (Rel. 36, Last
15-JUN-2002 (Rel. 41, Last
Chloroplast 30S ribosomal
                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00189; Ribosomal_S3_C; 1.
Pfam; PF00417; Ribosomal_S3_N; 1.
TIGRFAMS; TIGR01009; rpsC_bact; 1.
PROSITE; PS50823; KH_TYPE_2; FALSE_NEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE-97303241;
                            SEQUENCE FROM N.A.
                                                   NCBI_TaxID=3077;
                                                                                     Chloroplast
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"The sequence of the maize plastid encoded rps3 locus.";
Nucleic Acids Res. 15:4689-4689(1987).
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NCBI_TaxID=4577;
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                                                                                                                                                                                                                                                                                                                                   224 AA;
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                                                                                                                                                                                  STANDARD;
       Tamiya;
PubMed-9159184;
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66.7%;
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Last annotation update)
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Pred. No. 95;
2; Mismatches
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RESULT 14
RR3_ORYSA
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Best Local
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InterPro; IPR001351; Ribosomal_S3.
Pfam; PF00189; Ribosomal_S3_C; 1.
Pfam; PF00417; Ribosomal_S3_N; 1.
TIGRPAMS; TIGR01009; TPSC_bact; 1.
PROSITE; PS50823; KH_TYPE_2; 1.
PROSITE; PS00548; RIBOSOMAL_S3; 1.
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P12146;
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Inamura A., Yoshinaga K., Sugiura M.;
"Complete nucleotide sequence of the chloroplast green alga Chlorella vulgaris: the existence of ginvolved in chloroplast division.";
Proc. Natl. Acad. Sci. U. S. A. 94:5967-5972(1997).
I. SIMILARITY: BELONGS TO THE S3P FAMILY OF RIBO.
I. SIMILARITY: CONTAINS 1 KH TYPE-2 DOMAIN.
                                                                                                                                                  Hiratsuka J., Shimada H., Whittier R., Ishibashi T., Sakamoto M., Mori M., Kondo C., Honji Y., Sun C.-R., Meng B.-Y., Li Y.-Q., Kanno A., Nishizawa Y., Hirai A., Shinozaki K., Sugiura Nishizawa Y., Hirai A., Shinozaki K., Sugiura Chloroplast genome: "The complete sequence of the rice (Oryza sativa) chloroplast genome: intermolecular recombination between distinct tRNA genes accounts for a major plastid DNA inversion during the evolution of the cereals.";
                                                                                              a major plastid DNA inversion during the evolution Mol. Gen. Genet. 217:185-194(1989).
-i- SIMILARITY: BELONGS TO THE S3P FAMILY OF RIBOSC-i- SIMILARITY: CONTAINS 1 KH TYPE-2 DOMAIN.
                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT 1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Chloroplast 30S ribosomal protein S3.
                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
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                                                                                                                                                                                                                                                                            STRAIN-CV.
                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=4530;
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              by non-profit institutions as long
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2; Mismatches
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Pred. No.
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P73314;
01-NOV-1997
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16-OCT-2001
                                                            InterPro; IPR004088; KH_type_1.
InterPro; IPR001351; Ribosomal_S3.
Pfam; PF00013; KH-domain; 1.
Pfam; PF00189; Ribosomal_S3_C; 1.
Pfam; PF00417; Ribosomal_S3_N; 1.
                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                      Nation A., Muraki A., Nakazaki N., Naruo K., Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M., Tabata S.;
"Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.";
DNA Res. 3:109-136(1996).
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Pfam; PF00189; Ribosomal_S3.C; 1.

Pfam; PF00417; Ribosomal_S3.N; 1.

TIGRFAMs; TIGR01009; rpsC_bact; 1.

PROSITE; PS50823; KH_TYPE_2; FALSE_NEG.

PROSITE; PS00548; RIBOSOMAL_S3; 1.

RIBOSOMAL_S3; 1.

RIBOSOMAL_S3; 1.
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01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
30s ribosomal protein S3.
RPSC OR RPS3 OR SLL1804.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                 SMART; SM00322; KH; 1.
TIGREAMS; TIGR01009; r
                                                                                                                                                                                     EMBL; D90905; BAA17343.1;
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Kaneko T., Sato S., Kotani_H., Tanaka A., Asamizu E., Nakamura
                                                                                                                                                    InterPro; IPR004044; KH_TYPE_2.
InterPro; IPR004087; KH_dom.
                                                                                                                                                                  InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Cyanobacteria; Chroococcales; Synechocystis
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                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: THIS PROTEIN IS INVOLVED IN THE BINDING OF INITIATOR MET-TRNA (BY SIMILARITY).
; TIGR01009; rpsC_bact; 1. ps50823; KH_TYPE_2; 1. ps00548; RIBOSOMAL_S3; 1.
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SEQUENCE 239 AA; 27016 MW; 0664CE072B38C6B2 CRC64;
199 IKVWIF 204
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  671580 seqs, 206047115 residues
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Q1997 caenorhabdi
Q9kcw4 bacillus ha
Q9moc7 arabidopsis
Q9zv45 arabidopsis
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Q93hd9 streptomyce
Q9pmp4 campylobact
Q8rp)4 desulfitoba
Q9cu03 mus musculu
Q9mti7 oenothera h
Q8s8v5 atropa bell
O66753 aquifex aeo
Q9p3r7 neurospora
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13 J	275 IQVWIF 280	1 IQIWIF 6	Ouery Match 97.1%; Score 33; DB 8; Length 282; Best Local Similarity 83.3%; Pred. No. 1e+02; Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	SEQUENCE 282 AA; 33871 MW; 89CC910DAA22DFB2 CRC64;	Pfam; PF00189; Ribosomal_S3_C; 1.	InterPro; IPR001351; Ribosomal_S3.	Nucleic Acids Res. 26:5190-5198(1998). EMBL; D89861; BAA36537.1;	nucleotide sequence.";	uced from	"Structure and organization of the mitochondrial genome of the	MEULINE=99030526; PubMed=9801318; Ohta N., Sato N., Kuroiwa T.;	STRAIN=10D;	SEQUENCE FROM N.A.	[1]	NCBI_TaxID=45157;	Eukaryota; Rhodophyta; Bangiophyceae; Cyanidioschyzon.	Mitochondrion.	Cyanidioschyzon merolae.	RPS3.	al protein S3.	(TrEMBLrel 20, Last	(Trembirel 10.	01-MAY-1999 (TrEMBirel, 10, Created)		OSZNY PRELIMINARY: PRT: 282 AA	LT 1

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                                                                            Complete proteome. SEQUENCE 360 AA;
                                                                                              "Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis."; Nucleic Acids Res. 28:4317-4331(2000).
                                                                                                                                                        STRAIN-C-125 / JCM 9153;
MEDLINE-20512582; PubMed-11058132;
Takami H., Nakasone K., Takaki Y.,
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NCBI_TaxID=86665;
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InterPro; IPR003003; 7TM_chemo2.
InterPro; IPR000168; 7TM_nematode.
Pfam; PF01604; 7tm_5; 1.
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Rhabditidae; Peloderinae;
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Putative small nuclear ribonucleoprotein E.
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MEDLIKE-20083487; PubMed=10617197;
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
Cronin L.A., Shen M., Vanaken S.E., Umayam L., Tallon L.J., Gill J.E.,
Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
Salzberg S.L., Fraser C.M., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thallana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eddicotyledons; core et
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AC005724; AAD08943.1; -. InterPro; IPR001163; snRNP_Sm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EU Arabidopsis sequencing project; Submitted (MAR-2000) to the EMBL/CEMBL; AL161576; CAB81026.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lamar B., Stoneking
Mayer K.F.X.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheop Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                          STRAIN=CV.
                                                                                                                                                                                     "Sequence and analysis of chromosome 2 thaliana.";
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                                                                    Lin X.;
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                                                                                                                   SEQUENCE
                                                                                                                                                                 Nature
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                                                                                        ROM N.A.
COLUMBIA;
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83.3%;
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Q9CLF4;
Q1-JUN-2001
01-JUN-2001
01-JUN-2002
                                                                                                                                                                                            O63853;
01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1999 (TrEMBLrel. 11, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation updat
                                          Beaton M.J., Roger A.J., Cavalier-Smith T.;
"Sequence analysis of the mitochondrial genome of Sarcophyton glaucum: conserved gene order among octocorals.";
J. Mol. Evol. 47:697-708(1998).
                                                                                                                                                                                     NADH
  MEDLINE=98210232;
Pont-Kingdon G.,
                       SEQUENCE OF
                                                                                  SEQUENCE FROM N.A.
MEDLINE=99065763; PubMed=9847412;
                                                                                                                              Eukaryota; Metazoa; Cnida
Alcyoniidae; Sarcophyton.
                                                                                                                                                    Mitochondrion.
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EMBL; AE006167; AAK03365.1; -.
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Nucleocapsid; Ribonuc
SEQUENCE 88 AA; 10
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291 AA; 3;
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protein PM1281.
450-495 FROM N.A.
10232; PubMed=9541536;
n G., Okada N.A., Macf
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  Macfarlane
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 J.L.,
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  Beagley C.T.,
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Matches 4; Conser
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Best Local Similarity
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Wolstenholme D.R.;
"Mitochondrial DNA of the coral Sarcophyton glaucum contains a gene for a homologue of bacterial MutS: a possible case of gene transfer from the nucleus to the mitochondrion.";
J. Mol. Evol. 46:419-431(1998)
-i- CATALLYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
EMBL; AF064823; AAC99651.1; -.
EMBL; AF064823; AAC16387.1; -.
EMBL; AF063192; AAC16387.1; -.
EMBL; AF063192; Oxidored_q1.
Pfam; PF00361; Oxidored_q1.
Pfam; PF00361; Oxidored_q1; 1.
PRINTS; PR01559; DUFFYANTIGEN.
                                                              01-OCT-2000
01-OCT-2000
01-DEC-2001
                                                                                                    Q9PMP4;
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Q93HD9;
01-DEC-2001
01-DEC-2001
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EMBL; AB070945; BAB69249 1; -
InterPro; IPR000515; BPD_transp.
Pfam; PF00528; BPD_transp; 1.
PROSITE; PS00402; BPD_TRANSP_INN_MEMBR; UNKNOWN_1.
SEQUENCE 320 AA; 34176 MW; DD3BC5AB26756426 CR
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01-MAR-2002 (TrEMBLrel.
ABC transporter.
             Campylobacter jejuni.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                           Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi (Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osono Kikuchi H., Shiba T., Sakaki Y., Hattori M.; "Genome sequence of an industrial microorganism Streptomy avermitilis: Deducing the ability of producing secondary
Campylobacter
                                     Possible polysaccharide CJ1413C.
                                                                                                                                                                                                                                                                                                                                                                   metabolites.",
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE=21477403; PubMed=11572948;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptomyces avermitilis.
Bacteria; Firmicutes; Actinobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mitochondrion; NAD; SEQUENCE 495 AA;
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                                                             (TrEMBLrel.) (TrEMBLrel.
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66.7%;
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83.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 32; DB 8;
Pred. No. 2.8e+02;
                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                       98:12215-12220(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
            subdivision;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptomycetaceae;
                                                protein
                                                                                                                 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Actinobacteridae; Streptomyces.
                                                                                                                                                                                                                               2.8e+02;
0;
                                                                                                                                                                                                                                                             DB 2;
                                                                                                                 AA
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                                                             update)
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         Campylobacter group;
                                                                                                                                                                                                                                                            Length 320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 495
                                                                                                                                                                                                                                                                                                                                                                                          Streptomyces
                                                                                                                                                                                                                                                                                       CRC64;
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                                                                                                                                                                                                                                   0;
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QRESULT 10
QREPJ
ID QREPJ
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Matches
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                                                                                                                                                                                                                                         Q9CU03;
Q9CU03;
01-JUN-2001
SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Davis J.K., Tiedje J.M.;
"Sequence and transcriptional analysis of reductive dehalogenase of Desulfitobacterium.";
                                                                                                                                                               01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
1700116B05R1k protein (Fragment).
1700116B05RIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OBRPJ4 PRELIMINARY; PRT; 719 AA.
OBRPJ4; PRT 719 AA.
OBRPJ4 7002 (TrEMBLrel. 21, Created)
O1-JUN-2002 (TrEMBLrel. 21, Last sequence update)
O1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 80.1 kDa protein
Desulfitobacterium hafniense.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

STRAIN-NCTC 11168;

MEDLINE-20150912; PubMed-10688204;

MEDLINE-20150912; PubMed-10688204;

Parkhill J. Wren B.W., Mungall K., Ketley J.M., Churcher C.,

Parkhill J., Wren B.W., Mungall K., Feltwell T., Holroyd S.

Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S.

Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,

Juagels K., Karlyshev A.V., Moule S., Pallen M.J., Van Vliet A.H.M.,

Quall M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,

Whitehead S., Barrell B.G.;

"The genome sequence of the food-borne pathogen Campylobacter je
                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
                                                                                                                                       Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases EMBL; AF403182; AAL87758.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. STRAIN-DCB-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia; Clostridiales; Peptococcaceae; Desulfitobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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Nature 403:665-668(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=49338;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AL139078; CAB73837.1; -.
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EQUENCE 719 AA; 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                       Chordata;
Rodentia;
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66.7%;
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83.3%;
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Pred. No. 3.4e-
1; Mismatches
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Pred. No.
                                                                                    Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B806F0F0F0F1D79B CRC64;
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0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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RESULT 12
Q9MTI7
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Best Local S
Matches 5
               Query Match
 Best Local Similarity
                                                                            InterPro; IPR004044; KH_TYPE_2.
InterPro; IPR001351; Ribosomal_S3.C; 1.
Pfam; PF00189; Ribosomal_S3.C; 1.
Pfam; PF00417; Ribosomal_S3.N; 1.
TIGREAMS; TIGR01009; rPSC_bact; 1.
PROSITE; PS50823; KH_TYPE_2; 1.
PROSITE; PS00548; RIBOSOMAL_S3; UNKN
                                            Chloroplast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Custincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshazki Y., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Hayagshizaki Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            RPS3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9MTI7;
01-OCT-2000 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T. Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
                                                                                                                                                                                                                               chromosome, representing plastome Eucenothera plastomes.";
                                                                                                                                                                                                                                                                             Hupfer H., Swiatek M
Chiu W.L., Sears B.;
                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE=20309318; PubMed=10852478;
                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid eurosids II; Myrtales; Onagraceae; Oenothera.
                                                                                                                                                                                                                                                                                                                                                                                                                            Chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9MTI7
                                                                                                                                                                                                Mol. Gen. Genet. 263:581-585(2000). EMBL; AJ271079; CAB67198.1; -.
                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=85636;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Oenothera hookeri (Hooker's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ribosomal protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
EMBL; AK018963; BAB31497.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=C57BL/6J; TISSUE=TESTIS; MEDLINE=21085660; PubMed=11217851;
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                                                                                                                                                                                                                                                             Complete nucleotide sequence of the Oenothera elata plastid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40 IRIWIF 45
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5; Conserv
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                                                 AA;
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                                                 24971 MW;
88.2%;
83.3%;
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83.3%;
                                                                                                                                                                                                                                                                                              Hornung
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15,
21,
                                                                                                                                                                                                                                                                                                                                                                                                                                           evening primrose).
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Score
Pred.
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Pred. No.
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                                                 B0B741F658B010BA CRC64;
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No;
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 DB 8;
3e+02;
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1.6e+02;
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                 Length 218;
                                                                                                                                                                                                                                              distinguishable
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RESULT 14
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Matches 5
 Query Match
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066753;
01-AUG-1998 (TrEMBLrel. 07, C
01-AUG-1998 (TrEMBLrel. 07, L
01-MAR-2002 (TrEMBLrel. 20, L
                         Complete SEQUENCE
                                                   InterPro;
PROSITE; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The nucleotide sequence of the plastid chromosome of Atropa beliadonna (deadly nightshade) and its comparison with that a Nicotiana tabacum with emphasis on sequence elements relevant microevolution.";
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ316582; CAC88082.1;
                                                                                                                         Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L., Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R., Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;

"The complete genome of the hyperthermophilic bacterium Aquifex apolicus".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2002 (TrEMBLrel. 21, 01-JUN-2002 (TrEMBLrel. 21, 01-JUN-2002 (TrEMBLrel. 21, Ribosomal protein S3.
                                                              Nature 392:353-388(1998).

EMBL; AE000690; AAC06709.1; -.

InterPro; IPR000053; Thiored.

InterPro; IPR000531; TonB_boxC.
                                                                                                                                                                                MEDLINE=98196666; PubMed=9537320;
                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                     NCBI_TaxID=63363;
                                                                                                                                                                                                                                                   Aquitex aeolicus.
Bacteria; Aquific
                                                                                                                                                                                                                                                                           GUA OR AQ_443
                                                                                                                                                                                                                                                                                        Glutaredoxin-like protein.
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; endicotyledons; core eudicots;

Asteridae; euasterids I; Solanales; Solanaceae; Atropa.
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Submitted (NOV-2001) to the EMBL/GenBank/DDBJ database
EMBL; AL389890; CAB97283.2; -.
InterPro; IPR005103; Glyco_hydro_61.
Pfam; PF03443; Glyco_hydro_61; 2.
SEQUENCE 246 AA; 26817 MW; 30E4F3436791A92A CRC64;
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01-OCT-2000 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B.,

Nyakatura G., Mewes H.W., Mannhaupt G.;

Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                           Neurospora crassa.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariales; Sordariaceae; Neurospora.
                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=5141;
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, Sequence 11, Application US/08969683A
; Patent NO. 6136576
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APPLICANT: GENENCOR INTERNATIONAL, INC.
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-892-8112
TELEPHONE: 302-773-0164
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 391 and no acids
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/030,601
APPLICATION NUMBER: 13, 1996
ATTORNEY/AGENT INFORMATION:
NAME: FLOYD, LINDA AXAMETHY
REGISTRATION NUMBER: 33,692
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MEDIUM TYPE: 3.50 ICHN DISKETTE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WORD FOR WINDOWS
SOFTWARE: MICROSOFT WORD VERSION 7.0A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/968,563
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CORRESPONDENCE ADDRESS:
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STRANDEDNESS: unl
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STEPHEN K. PICATAGGIO
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                                                                                                                                                                                                                                                                                    GPD1
                                                                                                                                                                                                                                                                                                                                  unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MARIA DIAZ-TORRES DONALD E. TRIMBUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHARLES E. NAKAMURA ANTHONY A. GATENBY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VASANTHA NAGARAJAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GREGORY M. WHITED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SHARON L. HAYNIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AMY (KUANG-HUA) HSU
RICHARD D. LA REAU
                                                                                                                                                                                                                                                                                                                  protein
                                                                                                                                                                                                                                                                                                                                                    unknown
                                                                                                                                                                                                                 85.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PONT DE NEMOURS AND COMPANY
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                                                                                                                                                                                                  Score 29; DB
Pred. No. 8.2e
3; Mismatches
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                                                                                                                                                                                                                 DB 3;
8.2e+02;
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                                                                                                                                                                                                                                 Length 391;
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US-09-297-928-7; Sequence 7, Application US/09297928; Patent No. 6358716; GENERAL INFORMATION:
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: 650-864-7620
TELEFAX: 650-845-6504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS: LENGTH: 391 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/2:
FILING DATE: 13-NOV-1997
APPLICATION NUMBER: 60/030,601
FILING DATE: 13-NOV-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/969,683A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Genencor International, Inc
STREET: 4 Cambridge Place
STREET: 1870 South Winton road
CITY: Rochester
                                                                                                                                                                                                                                                                                                                                                                       68 VQMWVF 73
                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
nes 3; Conserv
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TOPOLOGY: unl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: U
ZIP: 14618
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                      1 IQIWIF 6
                          CORRESPONDENCE ADDRESS:
ADDRESSEE: GENENCOR INTERNATIONAL,
STREET: 4 CAMBRIDGE PLACE
1870 SOUTH WINTON ROAD
                                                                                                                           LAREAU, RICHARD D.
TITLE OF INVENTION: METHOD FOR THE PRODUCTION OF
GLYCEROL BY RECOMBINANT
                                                                                                                                                                                              APPLICANT: BULTHUIS, BEN A.
GATENBY, ANTHONY
HAYNIE, SHARON L.
                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
            CITY: ROCHESTER
STATE: NEW YORK
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                                                                                                                                                                                                                   ANTHONY A.
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                                                                                                                 ORGANISMS
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J.2e+02;
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COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH

COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: MICROSOFT WINDOWS 95

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US-08-919-624-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                   COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/919,624
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc
STREET: 3174 Porter Dr.
                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: NEW HUMAN G-PROTEIN COUPLED
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                 FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                        CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                          ZIP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68 VQMWVF 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity les 3; Conserv
                                                                                                                                                                                                                                                           COUNTRY:
                                                      APPLICATION NUMBER:
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REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: CR-9981-P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-892-8112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/03602
FILING DATE: NOVEMBER 13, 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                          94304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 391 amino acids TYPE: amino acid STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/297,928 FILING DATE: 11-May-1999 CLASSIFICATION: <UNKnown>
Billings, Lucy J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 302-773-0164
TELEX: 6717325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: MICROSOFT WORD VERSION 7.0A
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Shah, Purvi
                                                                                                                                                                                                                                                           USA
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50.0%;
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Pred. No. 8.2e+02;
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US-09-025-151-18
; Sequence 18, Application US/09025151
; Patent No. 6187525.
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US-09-065-474-145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Saccharomyces cerevisiae US-09-025-151-18
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                                                                Sequence 145, Application US/09065474
Patent NO. 6063599
GENERAL INFORMATION:
APPLICANT: Tang, Liang
APPLICANT: Blehm, E. Scot
TITLE OF INVENTION: DIROFILARIA AND BRUGIA ANKYRIN
TITLE OF INVENTION: DEST THEREOF
NUMBER OF SEQUENCES: 171
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 18
LENGTH: 68
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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Best Local
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APPLICANT: Fromont, Micheline
APPLICANT: Fromont, Micheline
APPLICANT: Fromont, Micheline
APPLICANT: Rain, Jean-Chlistophe
TITLE OF INVENTION: FAST AND EXHAUSTIVE METHOD FOR SELECTING A PREY
TITLE OF INVENTION: INTEREST: APPLICATION TO THE CONSTRUCTION OF MAPS OF
TITLE OF INVENTION: INTERACTORS POLYPEPTIDES
FILE REFERENCE: 03495-0164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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CURRENT FILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: line
IMMEDIATE SOURCE:
LIBRARY: CARDN
CLONE: 282414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 433 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            162 ISIWIF 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity tes 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 415-U-
TELEPHONE: 415-845-4166
ADDRESSEE: Carol Talkington Verser,
ADDRESSEE: Heska Corporation
STREET: 1825 Share Point Drive
CITY: Fort Collins
                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
nes 3; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: sir
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50.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                          Score 28;
Pred. No.
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Pred. No. 8.9e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                           Length 68;
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RESULT 8
US-09-557-034-145
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; MOLECULE TYPE:
US-09-065-474-145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 145, Application US/09557034
Patent No. 6365569
GENERAL INFORMATION:
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 145:
SEQUENCE CHARACTERISTICS:
LENGTH: 287 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: HW-5-(
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11 LRIWIF 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE: 24-AP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 IQIWIF 6
                                   APPLICATION NUMBER: 09/065,474
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: HW-5-C1
                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: Windows 95 SOFTWARE: WordPerfect for Windows, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Tang, Liang
APPLICANT: Tang, E. Scot
TITLE OF INVENTION: DIROFILARIA AND BRUGIA ANKYRIN
PROTEINS, NUCLEIC ACID MOLECULES,
TELECOMMUNICATION INFORMATION: TELEPHONE: 970/493-7272
                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Conservative
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                                                                                                                                                                      APPLICATION NUMBER: US/09/557,034
FILING DATE: 21-Apr-2000
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                   STREET: 1825 Sharp Point Drive CITY: Fort Collins STATE: Colorado
                                                                                                                                                                                                                                                                                                                                                   ZIP: 80525
                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-APR-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Carol Talkington Verser, Ph.D. Heska Corporation
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Pred. No. 8.9e+02
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                                                                                                                                                                                                                                                     Version 7.0
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159 LRIWIF 164

1 IQIWIF 6

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; MOLECULE TYPE: US-09-031-485-2
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US-09-031-485-2
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   Query Match
Best Local S
Matches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/09031485 Patent No. 5824306
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Matches 4; Conserv
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APPLICANT: Tang,
APPLICANT: Blehm,
                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: DIR
TITLE OF INVENTION: PRO
TITLE OF INVENTION: USE
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 145:
SEQUENCE CHARACTERISTICS:
LENGTH: 287 amino acids
                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
                                                                                                                                                                                                                                                                      CLASSIFICATION: 530
PRIOR APPLICATION UDATA:
APPLICATION NUMBER: US/0
FILING DATE: 24-APR-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOTTWARE: WordPerfect for Windows,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                           NAME: Verser, Carol Talkington REGISTRATION NUMBER: 37,459 REFERENCE/DOCKET NUMBER: HW-5
                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Carol Talkington Verser,
ADDRESSEE: Heska Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 80525
                Local Similarity
                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
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                                                                                                                               LENGTH:
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                                                                                                           amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
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    Conservative
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Blehm, E. Scot
                                                                                                 linear
                                                                                protein
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                82.4%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82.48;
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 Score 28; DB Pred. No. 9.6e 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2;
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Pred. No. 8
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9.6e+02;
0;
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                                 Length 312;
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US-08-847-429A-2

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TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
; LENGTH: 312 amino acids
TYPE: amino acid
; TYPE: amino acid
; TYPE: linear
; MOLECULE TYPE: protein
US-08-847-429A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Watches 4; Conserve
                                                                                                                                                                                                                                                                                                                                                                                       US-09-065-474-2
                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 11
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Sequence 2, App. -
Sequence 2, App. -
Sequence 2, App. -
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Sequence 2, App. -
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Sequence 2, App. -
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APPLICANT: Tang, Liang
APPLICANT: Blehm, E. Scot
                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                            APPLICANT: Tang, Liang
APPLICANT: Blehm, E. Scot
TITLE OF INVENTION: DIROFILARIA AND BRUGIA ANKYRIN
TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES, AND
TITLE OF INVENTION: USES THEREOF
TUBER OF SEQUENCES: 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
CAPOL Talkington Verser, Ph.D.
ADDRESSEE: Heska Corporation
STREET: 1825 Sharp Point Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 1022 - CITY: Fort Collins STATE: Colorado
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: DIROFILARIA AND BRUGIA ANKYRIN TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES, TITLE OF INVENTION: USES THEREOF
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              159 LRIWIF 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 970/15
TELEPHONE: 970/484-9505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/847,429A FILING DATE: 24-APR-1997 CLASSIFICATION: 435
                                      COUNTRY:
                                                              CITY: Fort Collins
STATE: Colorado
                                                                                                     ADDRESSEE: Carol Talkington Verser, Ph.D ADDRESSEE: Heska Corporation STREET: 1825 Sharp Point Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 IQIWIF 6
                      80525
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66.7%;
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Pred. No. 9.6e+02;
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RESULT 12
US-09-557-034-2
US-09-557-034-2
; Sequence 2, Application US/09557034
; Patent No. 6365569
; GENERAL IMFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local (
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INFORMATION FOR SEQ ID NO:
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 312 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/065,474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: HW
TELECOMMUNICATION INFORMATION:
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                                                 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/557,034

FILING DATE: 21-Apr-2000

CLASSIFICATION: <UNKnown>
PRIOR APPLICATION: <UNKnown>
PRIOR APPLICATION INDMBER: 09/065,474

FILING DATE: <UNKnown>
ATTORNEY/AGENT INFORMATION:

NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459

REFERENCE/DOCKET NUMBER: HW-5-C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
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ses 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 IQIWIF 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Tang, Liang
APPLICANT: Tang, Liang
Blebm, E. Scot
TITLE OF INVENTION: DIROFILARIA AND BRUGIA ANKYRIN
PROTEINS, NUCLEIC ACID MOLECULES, AND
                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 80525
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acids
                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Carol Talkington Verser, Ph.D. Heska Corporation STREET: 1825 Sharp Point Drive
                                       TELEPHONE: 970/493-72
TELEFAX: 970/484-9505
                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Fort Collins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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66.7%;
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Pred. No. 9.6e+02;
2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 312;
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; TOPOLOGY: linear; ; MOLECULE TYPE: protein; ; SEQUENCE DESCRIPTION: SEQ ID NO: US-09-557-034-2
)ç
                                Query Match
Best Local Similarity
"hes 3; Conserve
                                                                                                                     ORGANISM: Staphylococcus epidermidis US-09-134-001C-3703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
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; SEQ ID NO 5503
; LENGTH: 413
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    В
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US-09-134-001C-5503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JS-09-134-001C-3703
                                                                                                                                                                                 APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5503, Appartent No. 63803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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PPLICANT: Lynn Doucette-Stamm et al

ITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: GTC-007

CURRENT APPLICATION NUMBER: US/09/134,001C

CURRENT FILING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: US 60/064,964

PRIOR PELICATION NUMBER: US 60/055,779

PRIOR FILING DATE: 1997-11-08

PRIOR FILING DATE: 1997-08-14
                                                                                                                                                              LENGTH: 496
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                    ENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                 quence 3703, Application US/09134001C
tent No. 6380370
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     . 1 IQIWIF 6
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                                                   Conservative
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50.0%;
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                                                                Score 28; DB 4;
Pred. No. 1.5e+03;
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Pred. No. 1.2e+03;
1; Mismatches (
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Pred. No. 9.6e+02
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Search completed: January
Job time : 10 secs
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US-09-134-001C-3275
                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3275
LENGTH: 591
TYPE: PRT
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                                                                                                                                                            Matches
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
                                                                             359 VNIWIF 364
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                                                                                                                                                          Local Similarity
les 4; Conserv
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66.7%;
                  3, 2003, 15:34:30
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Pred. No. 1.7e+03;
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Maximum Match 10
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    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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   /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/ECT_NEW_PUB.pep:*
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/cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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Listing first 45 summaries
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   GenCore version (c) 1993 - 2003
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US-09-849-626-313
US-09-849-626-3172
US-09-815-242-5172
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US-09-815-242-11596
US-09-815-242-11103
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US-09-789-561-169
US-09-864-761-47624
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(without alignments)
23.825 Million cell updates/sec
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Compugen
Sequence 331, App
Sequence 331, App
Sequence 331, App
Sequence 1136, App
Sequence 5172, Ap
Sequence 316, App
Sequence 11959, A
Sequence 11952, A
Sequence 11592, A
Sequence 495, App
Sequence 1254, App
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Sequence
Sequence
                                                                                                                                                                                          e 92, Appl
e 169, App
e 47624, A
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26	26	26	26	26	26	26	26	26	26	26	26	26	27	27	27	27	27	27	27	27	27	27	27	27	27
76.5	76.5	76.5	76.5	76.5	76.5	76.5	76.5	76.5	76.5	76.5	76.5	76.5	79.4	79.4		79.4	79.4	79.4	79.4		79.4			79.4	79.4
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Sequence 11887, A	Sequence 8, Appli	Sequence 5, Appli	Sequence 115, App	Sequence 130, App	9	Sequence 4, Appli	Sequence 13, Appl	Sequence 9, Appli	Sequence 197, App	Sequence 11, Appl	Sequence 790, App	Sequence 45734, A	Sequence 12286, A	559	Sequence 8, Appli	Sequence 12921, A	Sequence 12247, A	Sequence 5626, Ap	Sequence 14, Appl	Sequence 16, Appl	Sequence 6166, Ap	Sequence 1175, Ap	Sequence 2, Appli	Sequence 905, App	Sequence 298, App

ALIGNMENTS

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RESULT 2
US-09-789-561-169
; Sequence 169, Application US/09789561
; Patent No. US20020064818A1
; GENERAL INFORMATION:
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; LOCATION: (143)
; OTHER INFORMATION:
US-09-789-561-92
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US-09-789-561-92
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Best Local S
Matches 5
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APPLICANT: Ni et al
TITLE OF INVENTION:
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SEQ ID NO 92
                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: PZ043P1
CURRENT APPLICATION NUMBER: US/09/789.561
CURRENT FILING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: PCT/US00/24008
PRIOR FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: 60/152,317
PRIOR FILING DATE: 1999-09-03
                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 1999-09-03
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                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                          LENGTH: 179
TYPE: PRT
                                                                                                                                                                     Local Similarity
                                                                                                          86 INIWIF
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Pred. No. 1.7e
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1.7e+02;
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US-09-864-761-47624

; Sequence 47624, Application US/09864761

; Patent No. US20020048763A1
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PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PELING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
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SEQ ID NO 169
LENGTH: 261
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Best Local Similarity
Matches 5; Conserv
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APPLICANT:
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CURRENT FILING DATE: 2001-05-23
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PRIOR FILING DATE: 1999-09-03
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PRIOR FILING DATE: 1999-09-03
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PRIOR APPLICATION NUMBER: PCT/US00/24008
PRIOR FILING DATE: 2000-08-31
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CURRENT FILING DATE: 2001-02-22
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LOCATION: (225)
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OR APPLICATION NUMBER: PCT/US01/00665
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00668
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00663
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00662
OR APPLICATION NUMBER: PCT/US01/00662
OR FILING DATE: 2001-01-30
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83.3%;
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Pred. No. 2.4e+02;
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US-09-864-761-47624
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PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine
                                                                                                                                                         SOFTWARE: Fa
SEQ ID NO 331
LENGTH: 92
TYPE: PRT
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Best Local
                                                             Matches
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Best Local Similarity
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                      APPLICANT: Wang, Aijun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
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31
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                             1 IQIWIF 6
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IQVWLY 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION:
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Lodes, Michael
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                                                                                                                                                                                                                                                                                                                                  Fan, Liqun
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Mannion, Jane
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                                                             Conservative
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NN: EXPRESSED IN HBLLOO, SIGNAL = 2.5
NN: EXPRESSED IN FILLA, SIGNAL = 2.2
NN: EXPRESSED IN PILACENTA, SIGNAL = 1.1
NN: EXPRESSED IN BT474, SIGNAL = 1.1
NN: EXPRESSED IN BT474, SIGNAL = 1.1
NN: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1
NN: SWISSPROT HIT: P08578, EVALUE 2.00e-16
NN: SWISSPROT HIT: BF680487.1, EVALUE 6.00e-31
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Michael A.
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Pred. No.
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Pred. No. 1
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US-09-902-941-331

GENERAL INFORMATION:

Patent No.

331, Application US/09902941 o. US20020172952A1

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Best Local Similarity
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SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 331
LENGTH: 92
TYPE: PRT
ORGANISM: Homo sapiens
US-09-902-941-331
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Best Local S
Matches 3
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LENGTH: 92
TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 331, Application US/09849626 Publication No. US20020197669A1
                                                                                                                                                                                                                          APPLICANT: Wang, Aijun
APPLICANT: Wang, Tongtong
APPLICANT: Switzer, Anne
APPLICANT: Switzer, Anne
APPLICANT: Clapper, Jonathan
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIACNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C16
CURRENT APPLICATION NUMBER: US/09/849,626
CURRENT APPLICATION NUMBER: US/09/849,626
CURRENT FILING DATE: 2001-05-03
NUMBER OF SEQ ID NOS: 1926
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: MCNADD, ANDRIA AND METHODS FOR THE THERAPY TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER FILE REFERENCE: 210121.478C17
CURRENT APPLICATION NUMBER: US/09/902,941
CURRENT FILING DATE: 2001-07-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Bangur, Chaitanya
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 31
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                                    1 IQIWIF 6
IQVWLY 36
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Johnson, Jeffrey C.
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Vedvick, Thomas S.
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                                                                       Conservative
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Pred. No. 1.3e+02
                                                                       3; Mismatches
                                                                                        Score 28; DB 9;
Pred. No. 1.3e+02
                                                                                                        DB 9;
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                                                                     Indels
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RESULT 7

Query Match Best Local Similarity

82.4%; 50.0%;

Score 28; DB 10; Pred. No. 3.1e+02;

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; ORGANISM: Pseudomonas aeruginosa US-09-815-242-5172
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                                                                                                                                                                                                                                          PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
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Best Local Similarity 50...
"~hes 3; Conservative
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SEQ ID NO 1436
LENGTH: 95
TYPE: PRT
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                                                                                                         NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 5172
LENGTH: 228
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                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
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CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05988
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SED ID NOS: 1890
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APPLICANT: Steve Ruben
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/269,308 PRIOR FILING DATE: 2001-02-16
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                                                                                         TYPE: PRT
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Yamamoto, Robert T.
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50.0%;
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Pred. No. 1.4e+02;
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Length 228;
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APPLICANT: Zyskind, Judith
APPLICANT: Ohlsen, Kari L.
APPLICANT: Ohlsen, Kari L.
APPLICANT: Forsyth, John
PPLICANT: Froelich, Jamie M.
APPLICANT: Froelich, Jamie M.
PPLICANT: Froelich, Jamie M.
APPLICANT: Yumamoto, Robert T.
APPLICANT: Xu, H. Howard
ITILE OF INVENTION: GENES IDENTIFIED AS REQUIRED FOR PROLIFERATION IN
TITLE OF INVENTION: ESCHERICHIA COLI
FILE REFERENCE: ELITRA.001DV1
CURRENT FILING DATE: 2001-07-23
PRIOR APPLICATION NUMBER: 09/492/709
PRIOR APPLICATION NUMBER: 60/117,405
PRIOR FILING DATE: 2000-01-27
PRIOR FILING DATE: 1999-01-27
NUMBER OF SEQ ID NOS: 485
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 1999-12:
PRIOR FILING DATE: 1999-12:
NUMBER OF SEQ ID NOS: 481
SOFTWARE: FASTSEQ for Window; SEQ ID NO 319
SEQ ID NO 319
SEQ ID NO 319
LENGTH: 233
TYPE: PRT
ORGANISM: Escherichia coli
US-09-741-669-319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-912-020-386
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Best Local Similarity
"htches 3; Conserve
                                                                                                        US-09-912-020-386
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                                                                                                                                                                 SEQ ID NO 386
LENGTH: 233
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                                      Query Match
Best Local Similarity
                     Matches
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TITLE OF INVENTION: Genes identified as required
TITLE OF INVENTION: proliferation of E. coli
File REFERENCE: ELITRA. 0094
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CURRENT APPLICATION NUMBER: US/09/741,669
CURRENT FILING DATE: 2000-12-19
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                                                                                                                     TYPE: PRT
ORGANISM: E. Coli
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Ohlsen, Kari L.
                     Conservative
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1999-12-23
                                      82.4%;
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            3; Mismatches
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Pred. No. 3.2e+02;
3; Mismatches 0
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                                      Score 28; DB 10;
Pred. No. 3.2e+02;
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US-09-815-242-13969
; Sequence 13969, Application US/09815242
; Patent No. US20020061569A1
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US-09-815-242-10353
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US-09-815-242-10353
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APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
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PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
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Best Local :
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        APPLICANT: Yamamoto, Robert T.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
CURRENT FILING DATE: 2001-03-21
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CURRENT FILLING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 00/206,848
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PRIOR APPLICATION NUMBER: 60/191,078
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nes 3; Conserv
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Yamamoto, Robert T.
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Pred. No. 3.2e+02;
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; ORGANISM: Helicobacter pylori
US-09-815-242-11592
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Query Match
Best Local Similarity
Thes 3; Conserve
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PRIOR FILLING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILLING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILLING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILLING DATE: 2000-10-23
PRIOR FILLING DATE: 2000-10-23
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 11592
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NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 13969
LENGTH: 233
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CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
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PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
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TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
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09-815-242-13969
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OR FILLING DATE: 2000-10-23
OR APPLICATION NUMBER: 60/253,625
OR FILLING DATE: 2000-11-27
OR APPLICATION NUMBER: 60/257,931
OR FILING DATE: 2000-12-22
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Zyskind, Judith W.
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50.0%;
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              Score 28; DB 10; Length 234; Pred. No. 3.2e+02; 3; Mismatches 0; Indels
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Pred. No. 3.
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3.2e+02;
hes 0; Indels
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                                            APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                            APPLICANT:
                CURRENT APPLICATION NUMBER: US/09/738,626
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RESULT 14
US-09-815-242-11103
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US-09-738-626-3652
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/259,308
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
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; SEQ ID NO 11103
; LENGTH: 235
; TYPE: PRT
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                                                                                                                                                                                                      Sequence 3652, Application US/09738626 Publication No. US20020197605A1
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Best Local Similarity 50.0
Matches 3; Conservative
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                                              APPLICANT:
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TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
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                              APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           198 VKVWIF 203
                                                                                                                                                                                                                                                                                                                                                                                     1 IQIWIF 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 IQIWIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FastSEQ for Windows Version
ANDO, SEIKO
HAYASHI, MIKIRO
OCHIAI, KEIKO
YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
                                                                                                                                  MIZOGUCHI, HIROSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ohlsen, Kari L.
Zyskind, Judith W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yamamoto, Robert T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Carr, Grant J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wall, Daniel
Trawick, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Application US/09815242
                                                                                                                                                                                                                                                                                                                                                                                                                                                        82.4%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 28; I
Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                 1.2e+02;
1es 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 235;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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0;

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CURRENT FILING DATE: 2000-12-18

PRIOR APPLICATION NUMBER: JP 99/377484

PRIOR FILING DATE: 1999-12-16

PRIOR APPLICATION NUMBER: JP 00/159162

PRIOR APPLICATION NUMBER: JP 00/159162

PRIOR APPLICATION NUMBER: JP 00/280988

PRIOR FILING DATE: 2000-04-07

PRIOR APPLICATION NUMBER: JP 00/280988

PRIOR FILING DATE: 2000-08-03

NUMBER OF SEQ ID NOS: 7059

SEQ ID NOS: 7059

LENGTH: 293

TYPE: PRT

ORGANISM: Corynebacterium glutamicum

US-09-738-626-3652

Query Match
B2.4%; Score 28; DB 9; Length 293;
Best Local Similarity 50.0%; Pred. No. 3.9e+02;
Matches 3; Conservative 3; Mismatches 0; Indels

1 IOINIF 6

1 IOINIF 6

1 IOINIF 6

1 IOINIF 94

Search completed: January 3, 2003, 15:52:06

Job time: 4.77273 secs
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Title:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Minimum DB seq length: Maximum DB seq length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Post-processing:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         al number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rched:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-543-188A-27
38
1 WLVWIA 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gapop 10.0 ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A_Geneseq_101002:*

1: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*

2: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*

3: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*

4: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:*

5: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:*

6: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd
                                                                                                                                                                                                                                                                                                            /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1988.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1989.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1990.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                           /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT:*
/SIDS2/gcgdata/geneseg/geneseqp-embl/AA1999.DAT:*
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/SIDS2/gcgdata/geneseg/genesegp-embl/AA2002.DAT:*
                                                                                                              /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1996.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1997.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT:*
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/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1994.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query Match Length DB	Length	DB	ID	Description
1	38	100.0	6	23	AAU11850	Peptide ligand for
2	38	100.0	371	23	ABB47793	Listeria monocytog
ω	37	97.4	230	22	AAG89817	C qlutamicum prote
4	37	97.4	230	22	AAB76811	Corynebacterium ql
տ	35	92.1	70	22	AAU47680	Propionibacterium
თ	35	92.1	241	23	ABP27890	Streptococcus poly
7	34	89.5	49	23	ABG68706	Human prostate spe
80	34	89.5	80	22	AAM86002	Human immune/haema
9	34	89.5	162	22	AAU32492	Novel human secret
10	34	89.5	235	22	AAU57493	Propionibacterium

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11
32	32	32	32	32	32	32	32	32	32	32	32	32	သ	သ	ယ	ω ω	ယ	သ	<u>3</u> 3	သ	ω ω	ယ	မ	ယ	ω	သ	ω 3	<u>ω</u>	ω ω	ω	ω ω	34	34	34
•			•																•	•			•	•		•	•	•	•	•	•	9	89.5	9
153	153	153	149	139	128	115	105	95	89	84	75	32	735	504	497	472	396	362	362	329	296	185	185	171	171	162	145	132	95	78	38	676	420	288
21	21	21	22	13	15	20	23	21	22	23	21	20	22	22	20	22	22	17	15	22	22	21	21	21	21	21	22	22	23	22	21	20	22	22
AAG53000	AAG21898	AAG15863	AAM90245	AAR29009	AAR54053	AAY60396	ABP01702	AAG00323	AA002795	ABP02429	AAB09351	AAY11779	AAU36496	ABG10850	AAY37610	ABG24925	ABG26161	AAW02667	AAR48695	AAB96276	AAG98330	AAG60773	AAG55839	AAG60774	AAG55840	AAG55841	AAU53601	ABG10849	ABP07995	AAO02505	AAB51390	AAY35418	AAU35667	AAU42440
Arabidopsis thalia	Arabidopsis thalia	Arabidopsis thalia	Human immune/haema	p64-h2 protein pro	Sequence of the VL	Human normal bladd	Human ORFX protein	Human secreted pro	Human polypeptide	ORFX pa	Hepatitis GB virus	Human 5' EST secre	Pseudomonas aerugi	human diagn	Protein which is s	Novel human diagno	5		8						Arabidopsis thalia	Arabidopsis thalia	Propionibacterium	Novel human diagno	Human ORFX protein	ide	Human secreted pep	a pn	Haemophilus influe	Propionibacterium

ALIGNMENTS

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AAU11850
                                                                                                                                                                                                                                                                                                                                                                  RESULT 1
                                                                                                                                                                                                                        Prion protein; Prp; ligand; octapeptide motif; scrapie; prion-associated disease; Creutzfeldt-Jakob disease; Gerstmann-Straussler-Scheinker disease; fatal familial insomnia;
         WPI; 2002-061944/08
                                                                          05-APR-2000; 2000US-0543188
                                                                                                 05-APR-2001; 2001WO-US11150
                                                                                                                                                                                        chronic wasting disease.
                                                                                                                                                                                                   feline spongiform encephalopathy; bovine spongiform encephalopathy; transmissible mink encephalopathy; exotic ungulate encephalopathy;
                                                                                                                                                                                                                                                                     Peptide ligand for Prion protein, PrP, #25
                                                                                                                                                                                                                                                                                                                                         AAU11850 standard; peptide; 6
                               Hammond DJ,
                                                                                                                       18-OCT-2001.
                                                                                                                                              WO200177687-A2
                                                                                                                                                                    Synthetic
                                                                                                                                                                                                                                                                                              26-MAR-2002
                                                     VI TECHNOLOGIES INC
                               Wiltshire VR,
                                                                                                                                                                                                                                                                                             (first entry)
                               Carbonell R,
                                                                                                                                                                                                                                                                                                                                         A
                               Shen
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Query Match
Best Local Similarity
""" of the state of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Dussurget O, Chetouau...

Dussurget O, Chetouau...

Daniels J, Goebel W, Kreft J, Kum ...

Daniels J, Goebel W, Kreft J, Kum ...

Berche P.

Hain T, Berche P.

Total C.

Total 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a ligand of less than 6 kD that binds to a polypeptide containing the sequence GlyTyrGlyGlnProHisGlyGly (A) or an analogue that is the retro-inverso isomer of (A). The sequence A is an octapeptide motif from the prion protein (PrP). The ligands are identified by binding assays with the peptide (A) or peptides containing (A). The ligands are used for detecting prion proteins (or prions) in biological or environmental samples, e.g. for diagnosis, also for removing them from samples, for treating or retarding development of prion-associated diseases, especially Creutzfeldt-Jakob diseases (in latrogenic, new variant, familial or sporadic forms), but also gerstmann-Straussler-Scheinker disease, fatal familial insommia, scrapie, bovine or feline spongiform encephalopathy, transmissible mink or exotic ungulate encephalopathy, or chronic wasting disease. The present sequence is a ligand of the invention.
                                                                                                                                                                                                                                                                  WPI;
                                                                                                                      Genomic sequence for Listeria and prevention of Listeria and
                                                                                                                                                                                                                                                                                                                                                 Chakraborty T, Domann E,
Perez-Diaz J, Baquero F,
Maduenio E, De Pablos B,
Rose M, Voss H;
        Claim
                                                                                       and prevention related polyper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation; vitamin Bl2; bacterial infection; disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Buchrieser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (INSP ) INST PASTEUR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-APR-2000; 2000FR-0004629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-APR-2001; 2001WO-FR01118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Listeria monocytogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Listeria monocytogenes protein #497.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New ligands for prion proteins, useful for detection or removal or prions and for treating prion-associated diseases, recognize a specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 WLVWIA 6
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                                                                                                                                                                                                                                                              2002-010914/01.
        6;
                                                                                       polypeptides
    SEQ ID No 498;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Frangeul L, Couve E, Rusniok C, Fsihi H, Dehoux P; Chetouani F, Nedjari H, Glaser P, Kunst F, Cossart P; Soebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA; rnal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
192pp; French
                                                                                                                                   and
                                                                                                                                                                                                                                                                                                                                                                                    Hain T, Berche P, Ch
Garcia Del Portillo F,
Wehland J, Kaerst U,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                               monocytogenes, useful e.g. for drelated bacterial infections,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 38; |
Pred. No. 7
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7.8e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Charbit A, Durant L;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                               Gomez-Lopez N;
Entian K, Hauf
                                                                                                                                                                          for treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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The present invention provides a number sequences from the Coryneform bacterium

of nucleotide and protein Corynebacterium glutamicum.

These

Claim

17;

SEQ ID NO: 3571; 246pp + Sequence Listing; English

Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene

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RESULT 3
AAG89817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CC The present invention relates to the genome sequence of Listeria CC monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of CC monocytogenes and related organisms, and for studying genes in L. CC monocytogenes and related organisms, and for studying genetic CC polymorphisms and other genomes. The present sequence is a protein cC encoded by the genome sequence of the present invention. Proteins CC expressed from the genome sequence are useful for raising specific cantibodies, identification of L. monocytogenes and related organisms, and CC for biosynthesis and biodegradation, especially biosynthesis of vitamin CC Ell. The genome sequence and proteins encoded by it are also useful for cselecting compounds that regulate gene expression and cell replication CC and modulate L. monocytogenes-related diseases. In addition, the genome compositions for the treatment or prevention of infections by L. CC monocytogenes and related organisms.

CC Note: The sequence data for this patent did not form part of the printed CC connecytogenes and related organisms.
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Best Local S
Matches 6
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                        WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C glutamicum
  N-PSDB;
                                                                    Nakagawa S,
Tateishi N,
                                                                                                                                                                                         03-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                               EP1108790-A2
                                                                                                                                                                                                                                                                                                                                                                                                                           Corynebacterium
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                                                                                                                                                                                                                 07-APR-2000;
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                                                                                                                                        (KYOW ) KYOWA HAKKO KOGYO
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scification, but was obtained in electronic format directly from WIPO
ftp.wipo.int/pub/published_pct_sequences.
2001-376931/40.
DB; AAH65036.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    orm bacterium; amino acid acid synthesis.
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                                                                    Mizoguchi
Senoh A,
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2000JP-0280988.
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                                                                                                                                                                                                                                                                                                                                                                                                                           glutamicum
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                                                               H, Ando S, Hayashi M,
Ikeda M, Ozaki A;
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Pred No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             synthesis; vitamin; saccharide;
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1.5e+02;
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                                                                                            Ochiai K,
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Zelder O,

Haberhauer G;

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RESULT 4
AAB76811
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Matches
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09-JUL-1999
14-JUL-1999
14-JUL-1999
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14-JUL-1999
27-AUG-1999
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27-AUG-1999
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08-JUL-1999;
08-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Corynebacterium glutamicum; brevibacterium lactofermentum; MCT; membrane construction and membrane transport protein; petroleum spill; hydrocarbon degradation; gram positive aerobic bacterium; marker; identification; microorganism; fine chemical production; transformation; genome mapping; genetic engineering.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and cryanic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-JUL-1999;
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09-JUL-1999;
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99DE-1032124

99DE-1032125

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99DE-1032180

99DE-1032191

99DE-1032291

99DE-1032292

99DE-1032227

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99DE-1031454
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83.3%;
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Pred. No. 1.3e+02;
1; Mismatches (
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Best Local S
Matches 5
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31-AUG-1999
31-AUG-1999
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03-SEP-1999
03-SEP-1999
03-SEP-1999
03-SEP-1999
                     21-APR-2000;
02-JUN-2000;
07-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAF67743 to AAF68080 encode the Corynebacterium glutamicum membrane construction and membrane transport (MCT) proteins given in AAB76510 to AAB76847. The MCT nucleic acids and proteins are useful in the identification of microorganisms which can be used to produce fine chemicals, for modulating fine chemical production in C. glutamicum or related bacteria (e.g. Brevibacterium lactofermentum), the typing or identification of C. glutamicum or related bacteria, as reference points for mapping C. glutamicum genome, and as markers for transformation. AAF68082 and AAF68082 represent sequencing primers which are used in an example from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 200
N-PSDB;
                                                                                                                                                                                                                                                                                                                                                         SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 20; Page 1012; 1119pp;
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                                                                                                                                                                              01-NOV-2001
                                                                                                                                                                                                                                                                                 Propionibacterium
                                                                                                                                                                                                                                                                                                                                    dermatological;
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                     ; 2000US-199047P.
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; 2000US-216747P.
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99DE-1040833.
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                                                                                                                                                                                                                                                                                                                                    osteopathic;
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83.3%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                    neuroprotectant.
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DB 22; I 1.3e+02; ches 0;

Length 230;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic CC polypeptides. The proteins and their associated DNA sequences are used in CC the treatment, prevention and diagnosis of medical conditions caused by CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. CC presence is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention cc and determining the amount of bound protein in the sample. The CC polypeptides may be used as antisques in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and compression and activity of P. acnes proteins. The antibodies may also be used as CC diagnostic agents for determining P. acnes proteins, by CC enzyme linked immunosorbent assay (ELISA).

CC Note: The sequence data for this patent did not form part of the printed content of the province of the printed of the printed of the province of the printed of the printed of the province of the printed of the
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                                           27-OCT-2000;
24-NOV-2000;
07-MAR-2001;
                                                                                                                                      29-OCT-2001;
                                                                                                                                                                                     02-MAY-2002.
                                                                                                                                                                                                                                   W0200234771-A2
                                                                                                                                                                                                                                                                            Streptococcus agalactiae
                                                                                                                                                                                                                                                                                                                       Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; antiinflammatory; infection; vaccine; meningitis; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus polypeptide SEQ ID NO 4956.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-JUL-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABP27890 standard;
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(CHIR-) CHIRON SPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; SEQ ID No 8875; 1069pp; English
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es 5; Conserv
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DB; AASS9539.
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                                           ; 2000GB-0026333.
; 2000GB-0028727.
; 2001GB-0005640.
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e J, Zhang Y,
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, Jen S, Carter D;
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Pred. No. 78;
1; Mismatches
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. 78;
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RESULT 7
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Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS (Streptococcus/GAS (Streptococcus/GAS (Streptococcus/GAS (Streptococcus/GAS (Streptococcus/GAS), given in the specification. The proteins have antibacterial and antinfilammatory activity. (I), nucleic acids encoding (I), ABN66044-ABN71326 and antibacteriat bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (I) are used to detect Streptococcus in a biological sample. (I) is used to determine whether a compound binds to biological sample. (I) is used to determine whether a compound binds to U). A composition comprising (I) or a nucleic acid encoding (I), may be used as a vaccine or diagnostic composition. The disease caused by Streptococcus that is prevented or treated may be meningitis. Nucleic acids on the contractive of WPI; 2002-557831/59
                                                                                                                                                                                                                                                                                                                                  27-NOV-2000; 2000US-253176P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; prostate specific nucleic acid; PSNA; prostate cancer; prostate specific protein; cytostatic; non-cancerous prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human prostate specific protein DEX0293_75.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 3656; 4525pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Telford J,
Tettelin H;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GENO-) INST GENOMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              168 WLMWIA 173
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                                                                                         S, N
                                                                                                                                                                                                                                        DIADEXUS INC
                                                                                         Macina RA,
n S;
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83.3%;
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Pred. No. 2.8e+02;
Pred. No. 2.8e+02;
                                                                                                                                     Cafferkey R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           non-cancerous prostate disease;
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RESULT 8
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Matches
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   31-JAN-2000;
04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
18-APR-2000;
19-MAY-2000;
07-JUN-2000;
07-JUN-2000;
07-JUL-2000;
07-JUL-2000;
07-JUL-2000;
07-JUL-2000;
07-JUL-2000;
07-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diagnosing and monitoring the presence and metastases of prostate cancer in a patient (the kit comprising a risk of cancer or presence of cancer in a patient (the kit comprising a means for determining the presence of the PSNA or PSP in a sample of a patient) and a vaccine comprising the polypeptide or the nucleic acid encoding the polypeptide. The PSNA, PSP and anti-PSP antibody are useful for diagnosing and treating cancer in a patient (e.g. by gene therapy). The nucleic acid molecule and polypeptide are also useful as vaccines for treating cancer, particularly prostate cancer and non-cancerous prostate diseases. The present sequence is a PSP of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a new isolated prostate-specific nucleic acid (PSNA) molecule comprising the CDNA sequences appearing as ABK97574-ABK97642 which encode prostate specific proteins appearing as ABK97574-ABK97646, or a sequence hybridising to a PSNA or which has 60% sequence homology with a PSNA. Also included are a method of determining the presence of a PSNA in a sample, a vector comprising the PSNA, a host cell comprising the vector, producing the polypeptide encoded by a host cell comprising the vector, producing the polypeptide encoded by the PSNA, a method of determining the presence of a PSF in a sample,
                                                                                                                                                                                                                                                 17-JAN-2001;
                                                                                                                                                                                                                                                                               09-AUG-2001.
                                                                                                                                                                                                                                                                                                             WO200157182-A2
                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                          cytostatic; gene therapy; vaccine; metastasis.
                                                                                                                                                                                                                                                                                                                                                                                         Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                           Human immune/haematopoietic antigen SEQ ID NO:13595
                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-NOV-2001 (first entry)
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   2000US-0179065

2000US-0186628

2000US-0184664

2000US-0186350

2000US-018974

2000US-0199123

2000US-0199123

2000US-0205467

2000US-0214886

2000US-0215135

2000US-0216880

2000US-0216880

2000US-0216880
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Pred. No.
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01-DEC-2000;
01-DEC-2000;
05-DEC-2000;
05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
                                         Claim 11;
                                                Nucleic acids encoding useful for preventing, metastasis -
                                                                                 (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                   17-NOV-2000;
                                                                                                                                                                         17-NOV-2000;
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DB; AAK58783.
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human immune/hematopoietic antigen polypeptides, diagnosing and/or treating cancers and

NO 13595; 3071pp + Sequence Listing; English

AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis are treatment of diseases associated with inappropriate (I) expression. For that affect the activity of supplement the patients own polynucleotides may be used example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) 6 produce secreted inserting decreased and

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Best Local
                                                                                                                          The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and the proteins are useful in genetic vaccination, testing and the proteins are useful in genetic vaccination, testing and the proteins are useful in genetic vaccination, testing and the proteins are useful to produce the proteins.
                therapy, and can be used as nutritional supplements. They may be used increase stem cell proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or stimulation; as anti-inflammatory agents; a in treatment of leukaemias. AAUJ9510-AAUJ33304 represent the amino aci sequences of novel human secreted proteins of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAK64703 to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK54950 and AAM82169
                                                                                                                                                                                                                                                                                                                                                                       Claim
                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acids encoding a range of vaccination, testing and therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; vaccination; gene therapy; nutritional supplement; stem cell proliferation; haematopoiesis; nerve tissue regeneration; immune suppression; immune stimulation; anti-inflammatory; leukaemia
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26-JAN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the nucleic acids into a host cell and culturing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Liu C,
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66.7%;
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02-JUN-2000;
07-JUL-2000;
                                                                                                                     polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to
               at ftp.wipo.int/pub/published_pct_sequences
                             specification,
                                                        downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELLIA).
                                                                                                                                                                                                                                                                                                                                                         Example 1; SEQ ID No 18688; 1069pp; English.
                                                                                                                                                                                                                                                                                                                                                                                           treating acne vulgaris
                                                                                                                                                                                                                                                                                                                                                                                                            vaccinating against and
                                                                                                                                                                                                                                                                                                                                                                                                                            Propionibacterium acnes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
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                             The sequence data for this patent did not form fication, but was obtained in electronic format
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                                                                                                                                                                                                                                                                                                                                                                                                                            polypeptides and nucleic acids useful for
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Pred. No.
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                                                         pustulosis, hypertosis and osteomyelltis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA).
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        Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                    polypeptides. The proteins and their associated DNA sequences are use the treatment, prevention and diagnosis of medical conditions caused P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
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02-JUN-2000; 2000US-208841P.
07-JUL-2000; 2000US-216747P.
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                                                                                                                                                                                                                                                                                                                                                                                                          treating acne vulgaris
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-APR-2001; 2001WO-US12865
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Propionibacterium acnes immunogenic protein #3336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          182 WFVWIA 187
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, Jen S, Carter D;
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3.9e+02;
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                  The invention relates to antisense inhibitors of genes essential to CC prokaryotic cellular proliferation, their use in identifying the CC genes, their use in the discovery of novel antibiotics, the essential CC genes themselves and the encoded proteins. The prokaryotes used are CC Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The CC invention is also useful for the identification of potential new targets (for antibiotic development. The antisense nucleic acids can also be used CC to identify proteins used in proliferation, to express these proteins, CC and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery CC programmes. The antisense nucleic acid sequence is also useful to screen CC a wide variety of organisms. The present sequence represents an CC essential prokaryotic cellular proliferation protein.

CC Note: The sequence data for this patent did not form part CC frant directly from WIPO at the printed specification, but was obtained in electronic
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AAU35667
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Best Local Similarity
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23-MAY-2000; 2000US-2056848P.
26-MAY-2000; 2000US-207727P.
23-OCT-2000; 2000US-242578P.
27-NOV-2000; 2000US-253655P.
22-DEC-2000; 2000US-25931P.
16-FEB-2001; 2001US-269308P.
                                                                                                                                                                                                                                                                                  New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antisense; prokaryotic cellular proliferation protein; antibiotic; antibacterial; drug design.
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Xu HH;
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RESULT 13
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                                                                                                                                                                                               C. pneumoniae causes respiratory disease such as pneumonia and bronchitis and is thought to be a contributing factor in heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema nodosum or pharyngitis. The polypeptides encoded by the open reading frames of the C. pneumoniae genome (see AAY34584-Y35879) can be used in immunogenic compositions as vaccines. Vectors containing C. pneumoniae nucleotides sequences can also be used as immunogenic compositions, especially where the vector directs the expression of a neutralising epitope of C. pneumoniae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genome sequence of Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-357842/30
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21-NOV-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis; sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine; neutralising epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chlamydia pneumoniae cellular envelope protein
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481 WLVWI 485
                                                                             Local Similarity hes 5; Conserv
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                                                                               Conservative
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97FR-0014673
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                                                                                                89.5%;
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                                                                                                  Score 34; pred. No.
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7e+02;
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                                                                                                                                                                                                                                                  RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rhowmatchia anaemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequences AAB51380-B51423 represent the amino acid sequences of 45 human secreted proteins encoded by the genes AAC93310-C9354. The genes and proteins are useful for preventing, ameliorating or treating medical conditions, e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer, and other cancers of the adrenal gland, bone, bone marrow breast astroitestinal tract lives along the process of the cancer.
Human polypeptide SEQ ID NO 16397.
                                                               06-NOV-2001
                                                                                                                                                                                     AAO02505 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              epilepsy; and and parasitic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             colitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid molecules encoding 45 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives -
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07-JAN-2000;
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cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cytostatic; immunosuppressive; nootropic; antiallergic; hepatotropic; antidiabetic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HUMA-) HUMAN GENOME SCI INC.
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                                                                                                                                                                                                                                                                                                                                           16 WLVWV 20
                                                                                                                                                                                                                                                                                                                                                                                                        1 WLVWI 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       itis; (c) cardiovascular disorders such as myocardial ischaemias; wound healing; (e) neurological diseases e.g. cerebral anoxia and lepsy; and (f) infectious diseases such as viral, bacterial, funga.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000-611720/58
DB; AAC93320.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       's disease, multiple sclerosis, rheumatoid arthritis and ulcerative
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                          Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immundisorders -
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RESULT 2 AE1548 AE1548 C:Species: Listeria innocua C:Species: Listeria innocua C:Date: 27-Nov-2001 #Sequence_revisi C:Accession: AE1548 R:Glaser, P.; Frangeul, L.; Buchries: Dominguez-Bernal, G.; Duchaud, E. Jonninguez-Bernal, G.; Duchaud, E. Jones, L.M.; Karst, U. Science 294, 849-852, 2001 A;Authors: Kreft, J.; Kuhn, M.; Kunsok, C.; Schlueter, T.; Simoes, N.; T. A;Title: Comparative genomics of Lista; Reference number: AB1077; MUID:215 A;Reference number: AB1077; MUID:215 A;Refacule type: DNA A;Residues: 1-371 <gla> A;Residues: 1-371 <gla> A;Experimental source: strain Clip11</gla></gla>	RESULT 1 ABI190 probable membrane protein lmo0925 C;Species: Listeria monocytogenes C;Date: 27-Nov-2001 #sequence_rev C;Accession: AE1190 R;Glaser, P; Frangeul, L; Buchr ; Dominguez-Bernal, G; Duchaud, D; Jones, L.M.; Karst, U. Science 294, 849-852, 2001 A;Authors: Kreft, J; Kuhn, M; R ok, C.; Schlueter, T; Simoes, N. A;Title: Comparative genomics of A;Reference number: AB1077; MUID: A;Accession: AE1190 A;Reference Finanary A;Molecule type: DNA A;Residues: 1-371 <gla> A;Cross-references: GB:NC_003210; A;Cross-references: GB:NC_003210; A;Experimental source: strain EGC C;Genetics: A;Gene: lmo0925 Query Match Best Local Similarity 100.0%; Best Local Similarity D0.0%; Matches 6; Conservative Qy 1 WLTWIA 518</gla>	30 33 86.8 355 31 33 86.8 391 32 33 86.8 436 33 86.8 527 35 33 86.8 594 36 33 86.8 594 37 33 86.8 692 39 33 86.8 692 40 33 86.8 692 41 33 86.8 692 42 33 86.8 692 42 33 86.8 1411 44 32 84.2 170
<pre>lin0925 (imported] - Listeria innocua (strain Clip11262) ta ince_revision 27.Nov-2001 #text_change 27.Nov-2001 ; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Blo uchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsih which the complete of /pre>	<pre>lmo0925 [imported] - Listeria monocytogenes (strain EGD-e) /togenes nce_revision 27-Nov-2001 #text_change 27-Nov-2001 ; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloed puchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A. loes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehl ics of Listeria species. ; MUID:21537279; PMID:11679669 ; MUID:21537279; PMID:11679669 100.0%; Score 38; DB 2; Length 371; 100.0%; Pred. No. 45; ive 0; Mismatches 0; Indels 0; Gaps 0;</pre>	hypothetical prote hypothetical prote prote critical prote acyltransferase, p acyltransferase, p hypothetical prote sensor protein Uhp hypothetical protein Uhp 28 2 731824 hypothetical protein Uhp hypothetical protein Uhp hypothetical protein Uhp hypothetical protein Hypothetical protein Hypothetical protein Hypothetical protein Hypothetical protein thiologis 2 H87275 hypothetical protein H15 2 H83294 hypothetical protein Hyp

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Nakazaki, N.; Shimpo, S.; Sugimoto, M., Almana.....
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DNA Res. 8, 205-213, 2001
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A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium And A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium And A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium And A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium And A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium And A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium And A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium And A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium And 
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A:Residues: 1-719 <KUN-
A:Coss-references: GB:AE006469; PIDN:AAK65164.1; PID:g14523607; GSPDB:GN00165
A:Experimental source: strain 1021, megaplasmid pSymA
R:Gallbert, F:; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barlo
Pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisl
L: Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.,
hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K
A:Title: The composite genome of the legume symbiont Sinornizobium mediloti.
A:Reference number: A36039; MUID:21368234; PMID:11474104
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C;Accession: AF2493
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.;
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.;
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                                                                                                                                                                                                                             A; Experimental source: strain
                                                                                                                                                                                                                                                                                 A;Cross-references: GB:BA000020; PIDN:BAB78210.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary
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A;Gene: lin0925
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30-Jun-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , F.; Barloy-Hubler N.A.; Fisher, R.F.
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RESULT
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WLLWIA 14

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probable symporter STY0171 [imported] - Salmonella enterica subsp.
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 27-C;Accession: AD0521
                                                                                                   A; Map position: 4
A; Introns: 36/1; 74/2; 100/1;
C; Superfamily: Caenorhabditis
                                                                                                                                                                                                                      A;Status: preliminary; translated from A;Molecule type: DNA A;Residues: 1-536 <WIL>
                                                                                                                                                                                                                                                                     submitted to the EMBL Data Library, A;Reference number: Z19317 A;Accession: T20736
                                                                                                                                                                                                                                                                                                                                      hypothetical protein F11A10.5 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #te: C;Accession: T20736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.;
A;Title: Complete genome sequence of a multiple drug resistant
A;Reference number: ABO502; PMID:11677608
A;Accession: ADO521
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                                                                                                                                                                     C; Genetics:
                                                                                                                                                                                     A;Cross-references: EMBL:268297; PIDN:CAA92595.1; GSPDB:GN00022; CESP:F11A10.5 A;Experimental source: clone F11A10
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A;Molecule type: DNA
A;Residues: 1-468 <PAR>
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C;Superfamily: melibiose
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R;Parkhill, J.; Dougan,
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N.; Farr
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phosphate transport system permease PstA - Aquifex C;Species: Aquifex aeolicus C;Date: 08-May-1998 #sequence_revision 08-May-1998 C;Accession: E70473
                                                                                  A;Title: The complete genome A;Reference number: A70300; NA;Accession: E70473
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E70473
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T19814
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct.1999 #sequence_revision 15-Oct.1999 #text_change 17-Mar-2000
C;Accession: T19814
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A;Title: Complete sequence analysis of the genome of the bacterium Mycoplasma A;Reference number: S73327; MUID:97105885; PMID:8948633
A;Accession: S73854
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Cross-references: GB:AE000768; NID:g2984249; PIDN:AAC07781.1; PID:g2984254; GB:AE00069
                       A; Molecule type: DNA
A; Residues: 1-285 < AQF>
                                                               A; Status: preliminary; nucleic acid
                                                                                                                                                                                      R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox,
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A; Introns: 17/2; 97/2;
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A; Note: the nucleotide
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                                                                                                                                                 Nature 392, 353-358, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:Z93375; PIDN:CABO7562.1; GSPDB:GN00020; CESP:C38C6.2
A;Experimental source: clone C38C6
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A; Residues: 1-585 <WIL>
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A;Accession: T19814
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A; Residues: 1-565 <HIM>
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lucosidase; alpha-amylase core
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66.7%;
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66.7%;
                                                                                                   of the hyperthermophilic bacterium Aquifex aeolicus MUID:98196666; PMID:9537320
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Pred. No. 1.9e+02;
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RESULT 10
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C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: G72310
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A; Residues: 1-318 <ARN>
A; Cross-references: GB:AE001760; GB:AE000512; NID:g4981510; PIDN:AAD36065.1;
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C; Superfamily: phoW protein
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C; Superfamily: 4''-O-acyltransferase
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A;Experimental source: cosmid B1883
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A; Residues: 1-384 < PAR>
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A;Accession: T44870
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Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
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5; Conser
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the EMBL Data Library, April
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Pred. No. 1.5e+02;
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RESULT 13
C85044
                                                                                                              A; Molecule type: DNA
A; Residues: 1-703 <ARN>
                                                                                                                                                                                                                            R;Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Nature Genet. 21, 385-389, 1999
A;Title: Comparative genomes of Clamydia pneumoniae and C. trachomatis. A;Reference number: A72000; MUID:99206606; PMID:10192388
                                                                                                                                                                                                                                                                                                                                                   thiol-disulfide interchange protein dsbD [imported] - Chlamydophila pneumoniae C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 28-Jul-2000 C;Accession: H72034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana A;Reference number: A85001; MUID:20083488; PMID:10617198 A;Accession: C85044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein AT4903490 [imported] - Arabidopsis thaliana C:Species: Arabidopsis thaliana (mouse-ear cress) C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001 C:Accession: C#5044 C:Accession: C#5044 R:anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Rature 402, 769-777, 1999
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A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A;Reference number: A64000; MUID:95350630; PMID:7542800
A;Accession: A64132
                                                       A; Experimental
                                                                                  A;Cross-references: GB:AE001660; GB:AE001363; NID:g4377095; PIDN:AAD18924.1; PID:g437709
                                                                                                                                                                        A; Status: preliminary
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C;Accession: A64132
                                                                                                                                                                                                      A; Accession: H72034
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A; Residues: 1-587 <STO>
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100.0%; Pred. No. 2.1e+02;
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Pred. No. 2.8e+02;
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thio, disulfide interchange protein [imported] - Chlamydophila pneumoniae (strain J138 C; Species: Chlamydophila pneumoniae, Chlamydia pneumoniae C; Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001 C; Accession: H86588 R; Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Nucleic Acids Res. 28, 2311-2314, 2000 A; Title: Comparison of whole genome sequences of chlamydia pneumoniae J138. A; Reference number: A86491; MUID: 20330349; PMID: 10871362 A; Accession: H86588
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                                                                                                                                                                                                       A;Gene: dsbD
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A;Molecule type: DNA
A;Residues: 1-703 <STO>
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(without alignments)
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                                                                                                                                                                                                                                                            pseudomonas
aeromonas h
vibrio chol
                                                                                                                                                                                 haemophilus
haemophilus
haemophilus
buchnera ap
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brucella me
aquifex aeo
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bordetella
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spiroplasma
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petunia hyb
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escherichia
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fusarium s
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TD08_MYCPN STANDARD; PRT; 565

ID YD08_MYCPN STANDARD; PRT; 565

AC P75472; 008088;
DT 16-0CT-2001 (Rel. 40, Created)
DT 16-0CT-2001 (Rel. 40, Last sequence updat
DT 16-0CT-2001 (Rel. 40, Last annotation upd
PAGE COCCACA CARRARARARARA RABERTO COCCACACA COCCACA COCACA                                                                                                                                                                                                                       EMBL;
                                                                                                                                                                 Hypothetical TRANSMEM
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                                                                                                                                                                                                    InterPro;
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VGL2_IBVK	VGL2_IBVB	VGL2_IBVD2	BOSS_DROME	TLR2_MACFA	TLR2_HUMAN	MAE1_SCHPO	TRI5_MYRRO	TRI5_STACH	TRI5_GIBPU	G392_DROME	TRI5_FUSPO	
aviar	P11223 avian infec	aviar	P22815 drosophila	Q95m53 macaca fasc	060603 homo sapien	P50537 schizosacch	Ol3489 myrothecium	O59947 stachybotry	P27679 gibberella	P58957 drosophila	Q00835 fusarium po	

ALIGNMENTS

update)

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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pneumoniae cytoskeletal protein HMW2 and cytadherence.";

J. Bacteriol. 179:2668-2677(1997).

-i- SUBCELLULAR LOCATION: Integral membrane protein (Potential).

-i- SIMILARITY: IN THE N-TERMINAL SECTION; TO M.PNEUMONIAE MPN095.

-i- SIMILARITY: IN THE C-TERMINAL SECTION; TO M.PNEUMONIAE MPN096.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-ATCC 29342 / M129;
MEDLINE-97252497; PubMed-9098066;
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STRAIN-ATCC 29342 / M129;
MEDLINE-97105885; PubMed-8948633;
Himmelreich R., Hilbert H., Plagens
                                                                                                                                                                                                                                                                          EMBL; AE000052; AAB96176.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mycoplasma pneumoniae.
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Complete sequence analysis of the genome of the bacterium Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Transposon mutagenesis reinforces the correlation between Mycoplasma
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Y986_THEMA
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Matches 4
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Best Local Similarity
Matches 5; Conserv
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16-OCT-2001
16-OCT-2001
16-OCT-2001
                     YG04_HAEIN STANDARD; PRT; 420 AA. P45268; O1-NOV-1995 (Rel. 32, Created) O1-NOV-1995 (Rel. 32, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update)
            Putative
                                                                                                                                                                                                                                                                          EMBL; AE001760; AAD36065.1; -.
TIGR; TM0986; -.
Hypothetical protein; Complete
SEQUENCE 318 AA; 36705 MW;
                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-99287316; PubMed-10360571;
Melson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
Haft D.H., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.
Sclewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson
Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O
Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
"Evidence for lateral gene transfer between Archaea and Bacteria
genome sequence of Thermotoga maritima.";
Nature 399:323-329(1999).

1- SIMILARITY: STRONG, TO E.COLI YFAT AND P.AERUGINOSA PA4490.
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thermotogaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Typothetical
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             phosphate
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482
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565
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(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
1 protein TM0986.
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Pred. No.
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ACC745B43D2184E2 CRC64;
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7041AB7510531380 CRC64;
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RESULT 4
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Cyanophora 
Cyanelle.
                                01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 3, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
ATP synthase B' chain (EC 3.6.3.14) (Subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                       ATPG.
                                                                                 P48085;
                                                                                            ATPX_CYAPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long modified and this statement is not removed.
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                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam;
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MEDLINE=95350630; PubMed=7542800;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae; Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein; Phosphate transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: BELONGS TO THE PHO-4 FAMILY OF TRANSPORTERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -! - FUNCTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Science 269:496-512(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                         Inner membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Whole-genome random sequencing and assembly of Haemophilus influenzae
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Best Local (
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15-JUN-2002 (Rel. 41,
15-JUN-2002 (Rel. 41,
Phosphate transport s
PSTA OR YPO4115.
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STRAIN=CO-92 / Biovar Orientalis;

MEDLINE=21470413; pubMed=11586350;

Parkhill J., Wren B.W., Thomson N.R., T

Prentice M.B., Sebaihia M., James K.D.,

Baker S., Basham D., Bentley S.D., Broo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Loeffelhardt W., Stirewalt V.L., Michalowski C.B., Annarella Farley J.Y., Schluchter W.M., Chung S., Newmann-Spallart C., Steiner J.M., Jakowitsch J., Bohnert H.J., Bryant D.A.; "The complete sequence of the cyanelle genome of Cyanophora the genetic complexity of a primitive plastid."; (In) Schenk H.E.A., Herrmann R., Jeon K.W., Mueller N.E., Schwerter W. C.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -i- FUNCTION: THE B'-SUBUNIT IS A DIVERGED AND DUPLICATED FORM B FOUND IN PLANTS AND PHOTOSYNTHETIC BACTERIA.
-i- CATALYTIC ACTIVITY: ATP + H(2)0 + H(+)(In) = ADP + phosphat
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NCBI_TaxID=2762;
                                                                    SEQUENCE FROM N.A.
                                                                                              NCBI_TaxID=632;
                                                                                                                       Yersinia pestis.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                 PSTA_YERPE
                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                       Hydrogen
                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Stirewalt V.L., Michalowski C.B., Loeffelhardt W., Bohnert H.J.,
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3; Conserv
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(Rel. 41, Last sequence update)
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ransport system permease protein p
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50.0%;
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13:327-332(1995).
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                                                                                                                       gamma
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Pred. No. 45;
3; Mismatches
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                                                                                                                       subdivision;
 K.D., Churcher C.
Brooks K., Cerde
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Springer-Verlag,
                                                                                                                                                                                                                                295
            Titball R.W., Holden M.T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (See http://www.isb-sib.ch/announce/
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PSTA_ECOLI
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Best Local :
sequence and c
J. Bacteriol.
[3]
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01-APR-1988
15-JUN-2002
                                                                                                                                                              SEQUENCE FROM N.A.

MEDLIND-85293094; PubMed-2993631;

Amemura M., Makino K., Shinagawa H., Kobaya

"Nucleotide sequence of the genes involved regulation of the phosphate regulon in Esch J. Mol. Biol. 184:241-250(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V., Leather S., Moule S., Oyston P.C.F., Quail M., Kutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G. "Genome sequence of Yersinia pestis, the causative agent of pla Nature 413:523-527(2001).
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                                   Surin B.P., Rosenberg H., Cox G.B.;
"Phosphate-specific transport system of Escherichia sequence and gene-polypeptide relationships.";
                                                                                                                                                                                                                                                                                                                                              Escherichia
                                                                                                                                                                                                                                                                                                                                                                                      PSTA OR PHOT
Escherichia
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TIGRFAMS; TIGR00974; 3a0107s02c;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: PART OF A BINDING-PROTEIN-DEPENDENT TRANSPORT SYSTEM FOR PHOSPHATE; PROBABLY RESPONSIBLE FOR THE TRANSLOCATION OF TI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation
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295 AA;
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(Rel. 41, Last annotation
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                                                                                                                                                                                           obayashi A., Nakata
lved in phosphate ti
Escherichia coli.";
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YA00_PYRHO
058728;
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                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00528; BPD_transp; 1.
TIGREAMS; TIGR00974; 3a0107s02c; 1.
PROSITE; PS00402; BPD_TRANSP_INN_MEMBR; 1.
Pransport; Phosphate transport; Transmembrane; Inner membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE000449; AAC76749.1; -. PIR; B23311; BVECPT. EcoGene; EG10782; pstA. InterPro; IPR000515; BPD_transp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X02723; CAA26508.1; -. EMBL; K01992; AAA24380.1; -. EMBL; L10328; AAA62077.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Webb D.C., Rosenberg H., Cox G.B.;
"Mutational analysis of the Escherichia coli phosphate-specific transport system, a member of the traffic ATPase (or ABC) family membrane transporters. A role for proline residues in transmembra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Burland V.D., Plunkett G. III, Daniels D.L., Blattner F.R.; "DNA sequence and analysis of 136 kilobases of the Escherichia coligenome: organizational symmetry around the origin of replication."; Genomics 16:551-561(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-K12 / MG1655;
MEDLINE-93315143; PubMed-7686882;
Burland V.D., Plunkett G. III, Da
                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
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                                                                                                                44
                                                                                                                                                                              Local Similarity
                                                                                                                                       1 WLVWI 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane SIMILARITY: BELONGS TO THE BINDING-PROTEIN-DEPENDENT TRANSPORT SYSTEM PERMEASE FAMILY. CYSTW SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3101. Chem. 267:24661-24668(1992).
FUNCTION: PART OF THE BINDING-PROTEIN-DEPENDENT TRANSPORT
FOR PHOSPHATE; PROBABLY RESPONSIBLE FOR THE TRANSLOCATION
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         (Rel. 40, Created)
(Rel. 40, Last sequence update)
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32321 MW;
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Best Local
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NUZC_NEPOL STANDAM.

16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-Jun-2002 (Rel. 41, Last annotation 2, chloroplast (EC 1.6.5.3).
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"Complete sequence and gene organization of the genome of a hyper-thermophilic archaebacterium, Pyrococcus horikoshii OT3.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use of the profit institutions as long as its content use of the profit institutions as long as its content use of the profit institutions as long as its content use of the profit institutions as long as its content use of the profit institutions as long as its content use of the profit institutions as long as its content use of the profit institutions as long as its content use of the profit institutions as long as lo
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STRAIN=NIES-484;
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                 MEDLINE=99398694; PubMed=10468594;
                                                                                                                Chlorodendrales;
                                                                                                                                          Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AP000004; BAA30097.1; -.
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Furmel M.,
                                                                                               NCBI_TaxID=31312;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical
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Otis C.,
                                                                                                                                        Viridiplantae;
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34 5,
34 10
55 7,
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212 23
240 26
274 29
310 3:
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"Ortein; Transmembrane;
"POTENTI!
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                                                                                                                       Chlorodendraceae;
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75
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Lemieux C.
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50.0%;
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Best Local S
Matches 4
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P10550; Q03092;
01-FEB-1995 (Rel. 31, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                    Barrell B.G., Badcock K., Bankier A.T., Bowman S., Brown D., Churcher C.M., Connor R., Copsey T., Dear S., Devlin K., Fraser Gentles S., Hamlyn N., Horsnell T., Hunt S., Jagels K., Jones Louis E., Lye G., Moule S., Moule T., Odell C., Pearson D., Rajandream M.A., Riles L., Rowley N., Skelton J., Smith V., Walsh S.V., Whitehead S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oxidoreductase; TRANSMEM 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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              Decottignies A., Lambert L., Catty P., Degand H., Epping E.A., Moye-Rowley W.S., Balzi E., Goffeau A.; "Identification and characterization of SNQ2, a new multidrug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF137379; AAD54809.1;
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Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                       Saccharomyces cerevisiae (Baker's yeast).
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                                                                   MEDLINE=95355421;
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                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                         [DENTIFICATION,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42 WLAWVA 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
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SUBCELLULAR LOCATION: Integral membrane protein. Chlor
SIMILARITY: BELONGS TO THE COMPLEX I SUBUNIT 2 FAMILY.
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                                                                                                                                                                                                                                                                                                                                      Ascomycota;
                                                                   PubMed=7629127
                                                                                                                                                                                                                                                                                                                      Saccharomycetaceae;
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STRAIN-ATCC 27894 / UTEX 581;
Wickrema A., Barrum S.R., Jaworski J.G.;
Submitted (JAN-1989) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; 238113; CAA86236.1; -. EMBL; Z46881; CAA86980.1; -. SGD; S0001275; PDR11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          '! SUBCELLULAR LOCATION: Integral membrane protein (Potential).
'! SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. PDR5 SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. Biol. Chem.
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PROSITE; PS00211; ABC_TRANSPORTER;
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This SWISS-PROT entry is copyright.
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01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Mercuric transport protein (Mercury ion trans
                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                        resistance (mer) oper
FEMS Microbiol. Rev.
                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=97309939; PubMed=9167257; Osborn A.M., Bruce K.D., Strike P., Ritchie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shewanella putrefaciens (Pseudomonas putrefaciens).
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                                                                                                                                                                                              EMBL; Z49196; CAA89054.1; -
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POTENTIAL.

HG(2+) (BY SIMILARITY).

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HG(2+) (BY SIMILARITY).
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       Gaps
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Query Match
Best Local S
Matches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAY-2000 (Rel. 3
30-MAY-2000 (Rel. 3
15-JUN-2002 (Rel. 4)
ER lumen protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09ZTN2;
30-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Isolation and characterization of cDNAs expressed in the early stages of flavonol-induced pollen germination in petunia."; plant physiol. 123:999-710(2000).

-i- FUNCTION: REQUIRED FOR THE RETENTION OF LUMINAL ENDOPLASMIC RETICULUM PROTEINS, DETERMINES THE SPECIFICITY OF THE LUMINAL PROTEIN SYSTEM. ALSO REQUIRED FOR NORMAL VESICULAR TRAFFIC THROUGH THE GOLGI. THIS RECEPTOR RECOGNIZES H-P-----SIMILARITY).
                                                  DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophy
Spermatophyta; Magnoliophyta; eudico
Asteridae; euasterids I; Solanales;
                                                                                                                                                                                                                                                               Prodom; PD005774; PROSITE; PS00951; PROSITE; PS00952;
                                                                                                                                                                                                                                                                                                                            EMBL; AF049922; AAD02548.1; -.
InterPro; IPR000133; ERret_receptor.
                                                                          TRANSMEM
                                                                                                   TRANSMEM
                                                                                                              DOMAIN
                                                                                                                          TRANSMEM
                                                                                                                                                   TRANSMEM
                                                                                                                                                                                                                                                   Endoplasmic
                                                                                                                                                                                                                                                                                                      PRINTS;
                                                                                                                                                                                                                                                                                                                   Pfam; PF00810;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Petunia hybrida (Petunia).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ERD2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ERD2_PETHY
                                                                                       DOMAIN
                                                                                                                                       DOMAIN
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                                                                                                                                                                                                                            TRANSMEM
                                                                                                                                                                            TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          110 WIVWFA 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 H
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: Integral membrane protein. SIMILARITY: BELONGS TO THE ERD2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | || | |
 Similarity
4; Conserv
                                                                                                                                                                                                                                                                                                    F00810; ER_lumen_recept; PR00660; ERLUMENR.
                                                                                                                                                                                                                                                                                          PD005774;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein retaining
                                                   215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 σ
  Conservative
                                                                                                                                                                                                                                                     reticulum;
                                                                                                                                                    36
54
62
83
                                                   AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                             53
61
82
98
112
113
119
119
119
110
120
202
215
25602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39,
41,
                                                                                                                                                                                                                                                               ERret_receptor; 1.
ER_LUMEN_RECEPTOR_1; 1.
ER_LUMEN_RECEPTOR_2; 1.
              84.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
uning receptor (HDEL receptor)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                  Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptophyta; Embryophyta; Tracheophyta, yta; eudicotyledons; core eudicots;
                                                    ME.
            Score 32;
Pred. No.
                                                  CYTOPLASMIC (POTENTIAL).
7A6E4EF4F017CF65 CRC64;
                                                                                                              CYTOPLASMIC (POTENTIAL).
                                                                                                                                                               CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                               CYTOPLASMIC (POTENTIAL)
                                                                                                   POTENTIAL
                                                                                                                                                                                                     POTENTIAL.
                                                                                                                                                                                                                               POTENTIAL
                                                                            POTENTIAL
                                                                                      LUMENAL (POTENTIAL).
                                                                                                                                       LUMENAL (POTENTIAL).
                                                                                                                                                    POTENTIAL.
                                                                                                                                                                                                                                         LUMENAL (POTENTIAL).
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 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Solanaceae;
                                                                                                                                                                                        (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              215 AA
                                                                                                                                                                                                                                                     Protein transport; Receptor
                83
                         DB
                        Length 215;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Petunia
   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (PGP169-12).
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  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 13
                                                         Query Match
Best Local
                                              Matches
                                                                                            DOMAIN
SEQUENCE
                                                                                                                                                                              TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Microbiology 146:3251-3257(2000).
-!- FUNCTION: Transport of water across the membrane. Possibly involved in the adaptation to variation in intravacuolar pl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BRUAB
                                                                                                                                                      TRANSMEM
REPEAT
                                                                                                                                                                                                                             TRANSMEM
                                                                                                                                                                                                                                       Transport;
                                                                                                                                                                                                                                                                TIGRFAMS;
                                                                                                                                                                                                                                                                        PRINTS; PR00783; MINTRINSICP. ProDom; PD000295; MIP_family; 1.
                                                                                                                                                                                                                                                                                                                         EMBL; AF148066; AAF73105.1; -. HSSP; P29972; 1H6I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brucellaceae; Brucella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brucella abortus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9LA79;
                                                                                                                                                                                                                 TRANSMEM
                                                                                                                                                                                                                                                     PROSITE;
                                                                                                                                                                                                                                                                                                    Pfam; PF00230; MIP;
                                                                                                                                                                                                                                                                                                                                                                                                                         between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rodriguez M.C., Froger A., Rolland J.-P., Thomas Delamarche C., Garcia-Lobo J.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-20553188; PubMed-11101683;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AQPZ OR AQPX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Aquaporin
                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brucella abortus."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AQPZ_BRUAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                       RANSMEM
                                                                                                                                                                                                                                                                                                              nterPro; IPR000425; MIP_family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5-JUN-2002
204
                                             Local Similarity nes 4; Conserv
                      1 WLVWIA 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        functional water channel protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBUNIT: Homotetramer (By similarity).
SUBCELLULAR LOCATION: Integral membrane protein. Inner memb
SIMILARITY: BELONGS TO THE MIP/AQUAPORIN FAMILY (TC 1.A.8).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                osmolarity.
WLFWVA 209
                                                                                                                                                                                                                                                                                                                                                                                                                    SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                     PS00221;
                                                                                                                                                                                                                                                               TIGR00861; MIP; 1.
                                                                                           92
228 AA;
                                                                                                                                                                                                                                         Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Aquaporin X).
                                              Conservative
                                                                                                                              34
81
127
154
203
63
184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                    MIP;
                                                                                                                              103
149
176
225
65
186
                                                                                            97
23145
                                                                                                                                                                                                                 56
                                                        84.2%;
66.7%;
                                                                                            WW;
                                                                                                                                                                                                                                       Inner membrane;
                                             ۲,
                                                        Score 32;
Pred. No.
                                                                                                                                                                             POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                          OF THE TETRAMER (BY SIMIL POLY-ALA. 23C64C39E4DD444A CRC64;
                                                                                                                                           NPA 1.
NPA 2.
                                                                                                                                                                  POTENTIAL.
                                                                                                                                                                                                                 POTENTIAL.
                                                                                                                                                                                                                           POTENTIAL.
                                                                                                                               INVOLVED IN TETRAMERIZATION OR STABILITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       in the pathogenic bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  228
                                                       DB
88;
                                                                                                                                                                                                                                                                                                                                                                                               There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A
                                                                                                                                                                                                                                       Repeat.
                                                                                                                  (BY SIMILARITY).
                                             1;
                                                                  Length 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Aguero
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                          restrictions
                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <u>-</u>
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                                           Gaps
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RESULT 14

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Query Match
Best Local Similarity
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Q9L772;
15-JUN-2002
                                         DOMAIN
SEQUENCE
                                                                                SITE
                                                                                                          TRANSMEM REPEAT
                                                                                                                                                                                                                                                                                               EMBL; AF226624; AAF36396.1; -. EMBL; AE009450; AAL51252.1; -. HSSP; P29972; 1H6I.
                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI the European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Brucella melitensis.";
Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
-!- FUNCTION: Transport of water across the meninvolved in the adaptation to variation in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=16M / ATCC 23456 / Biotype 1;
MEDLINE=20020109; PubMed=11756688;
MEDLIVECCHIO V.G., Kapatral V., Redkar R.J., Patra G., Mujer C., Los T.,
IVANOVA N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G.,
Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E.,
Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
Haselkorn R., Kyrpides N., Overbeek R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria;
Brucellaceae; Brucella.
                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Cloning and nucleotide sequence of aquaporin
melitensis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brucella melitensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Aquaporin Z.
AQPZ OR BMEI0070
                                                                                                                                                                                                                                          PRINTS; PR00783; MINTRINSICP. ProDom; PD000295; MIP_family;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: BELONGS TO THE MIP/AQUAPORIN FAMILY (TC 1.A.8).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SUBUNIT: Homotetramer (By similarity).-!- SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Suarez-Guemes F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hernandez-Castro R., Verdugo-Rodriguez A., Gutierrez-Pabello J.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=29459
                                                                                              REPEAT
                                                                                                                                                                                          TRANSMEM
                                                                                                                                                                                                      Transport;
                                                                                                                                                                                                                  PROSITE;
                                                                                                                                                                                                                                TIGRFAMS;
                                                                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The genome sequence of the facultative intracellular
                                                                                                                                     TRANSMEM
                                                                                                                                                 PRANSMEM
                                                                                                                                                               TRANSMEM
                                                                                                                                                                           TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                osmolarity (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (By similarity)
                                                                                                                                                                                                                                                                       PF00230; MIP;
                                                                                                                                                                                                                  PS00221; MIP;
                                                                                                                                                                                                                                TIGR00861; MIP; 1.
                                                                                                                                                                                                                                                                                 IPR000425; MIP_family.
                                     92
228
                                                                                                                                                                                         Transmembrane; 7 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Rel. 41, Created)
(Rel. 41, Last sequence update)
(Rel. 41, Last annotation update)
                                         AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                29
103
149
176
225
285
186
                                         97 I
23189 MW;
 84.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                    Inner membrane;
  Score
Pred.
                                                                                                                                               POTENTIAL. POTENTIAL.
                                                                  INVOLVED IN TETH OF THE TETRAMER
                                                      POLY-ALA
                                                                                                           NPA
                                                                                              NPA 2
                                                                                                                      POTENTIAL.
                                                                                                                                     POTENTIAL.
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                                                                                                                                                                                         POTENTIAL
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                                         64282C39E4DD4109 CRC64;
  No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  228 AA
                                                                  IN TETRAMERIZATION OR STABILITY
STRAMER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                (See http://www.isb-sib.ch/announce/
  DB 1;
88;
                                                                                                                                                                                                                                                                                                                                                                                       There are no restrictions on ong as its content is in no
                                                                                                                                                                                                    Repeat; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             membrane. Possibly in intravacuolar pl
                                                                                                                                                                                                                                                                                                                                                                             Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene of Brucella
             Length 228;
                                                                                                                                                                                                                                                                                                                                                                             bу
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pathogen
                                                                                                                                                                                                                                                                                                                                                                                and
                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL
                                                                                                                                                                                                                                                                                                                                                                                for
                                                                                                                                                                                                                                                                                                                                                                                                                                  collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                     outstation
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Search completed: January 3, 2003, 15:29:24 Job time: 6.18182 secs
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ID Y836_AQUAE
                                                                                                                                                                                                                                              uery Match
Sest Local Similarity
Watches 4; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein; Transmembrane; Complete proteome.
TRANSMEM 42 4 POTENTIAL.
TRANSMEM 42 62 POTENTIAL.
TRANSMEM 100 120 POTENTIAL.
TRANSMEM 145 165 POTENTIAL.
TRANSMEM 145 165 POTENTIAL.
TRANSMEM 171 191 POTENTIAL.
TRANSMEM 171 191 POTENTIAL.

B 934B56FEA35B183 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L., Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R., Feldman R.A., Short J.M., Olson G.J., Swanson R.V.; "The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.";
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16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Hypothetical protein AQ_836.
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183 WLVWL 187
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08z9f2 salmonella
0914i1 salmonella
019337 caenorhabdi
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08y063 ralstonia s
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RA Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA Longer L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
RA Mordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
RCOmparative genomics of Listeria species.";
Science 294.849-852(2001).
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O1-DEC-2001 (TrEMBLrel. 19,
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Hypothetical protein; Complete proteome.

SEQUENCE 371 AA; 41360 MW; 4EFE4A30E917C242 CRC64;
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STRAIN=CLIP 11262 / SEROVAR 6A;
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NCBI_TaxID=1642;
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Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,

Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,

Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,

Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,

Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,

Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,

Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,

Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,

Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;

"Comparative genomics of Listeria species.";

R EMBL; AL591977; CAC9903.1;

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01-MAR-2002
01-MAR-2002
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                   Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S., Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L., Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N., Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T., Siguier P., Thebault P., Whalen M., Wincker P., Levy M., Weissenbach J., Boucher C.A.;
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01-MAR-2002 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
                                                                                                                                                                                  MEDLINE=21681879; PubMed=11823852;
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MEDLINE-21537279; PubMed-11679669;
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Hypothetical protein; Complete proteome.
SEQUENCE 371 AA; 41252 MW; 54E7E86545CAA62E CRC64;
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transmembrane protein.
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Pred. No. 89;
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08XPT4;

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01-MAR-2002 (TrEMBLrel. 20, Created)

1 01-MAR-2002 (TrEMBLrel. 20, Last sequence

1 01-JUN-2002 (TrEMBLrel. 21, Last annotation of transmembrane TWO-component separation (EC 2.7.-.-).
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Q92ZH9;
Q1-DEC-2001
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Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P.,
Barnett M.J., Fisher R.F., Jones T., Capela D., Galibert F., Gouzy J.,
Barloy-Hubler F., Bowser L., Capela D., Galibert F., Gouzy J.,
Gurjal M., Hong A., Huizar L., Hyman R.W., Kahn D., Kahn M.L.,
Kalman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells
Yeh K.-C., Davis R.W., Federspiel N.A., Long S.R.;
"Nucleotide sequence and predicted functions of the entire
Sinorhizobium meliloti pSymA megaplasmid.";
Proc. Natl. Acad. Sci. U.S.A. 98:9883-9888(2001).
EMBL; AE007241; AAK65164.1; -.
                                                                                                                                                                                                                                                                                                                                          PROSITE;
Plasmid;
SEQUENCE
         Ralstonia.
NCBI_TaxID=305
                                                Ralstonia solanacearum (Pseudomonas Plasmid megaplasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rhizobium meliloti (Sinorhizobium meliloti). Plasmid pSymA (megaplasmid 1). Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae; Sinorhizobium.
                                      Bacteria;
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InterPro; IPR000504; RNA_rec_mot.
Pfam; PF00924; MS_channel; 1.
PROSITE; PS00030; RRM_RNP_1; UNKNOWN_1.
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EMBL; AL646063; CAD14883.1;
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                                                                                                                                                                                                                                     333 WLVWVA 338
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5; Conserv
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719 AA; 77245 MW; 045DDBCCB16917B9 CRC64;
                                    Proteobacteria;
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1 (TremBLrel. 19,
2 (TremBLrel. 21,
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83.3%;
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Last annotation update)
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Pred. No. 2
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Pred. No.
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                                                               solanacearum).
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2.4e+02;
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"Genome sequence of the plant pathogen Ralstonia solanacearum.";

Rature 415.497-502(2002).

REMBL; AL646085; CAD18704.1; -.

REMBL; A
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01-MAR-2002 (TrEMBLrel. 20, 1
Hypothetical protein Alr7126.
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"Complete genomic sequence of the filamentous recomplete genomic sequence gen
                                                                                                                                                                                                                                                      cyanobacterium Anabaena sp. strain DNA Res. 8:205-213(2001).
EMBL; AP003600; BaB78210.1; -
Plasmid; Hypothetical protein; Comp SEQUENCE 651 AA; 74404 MW; 6AB7
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01-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anabaena sp. (strain PCC 7120).
Plasmid pCC7120alpha.
Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc
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Transferase; Plasmid; Complete
SEQUENCE 438 AA; 46589 MW;
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Kaneko T., Nakamura Y., Wolk C.P.,
Watanabe A., Iriguchi M., Ishikawa
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ima K., Kimura T.,
A., Muraki A.,
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Crossgrove K., Laudet V., Maina C.v.;
Crossgrove K., Laudet V., Maina C.v.;
Crossgrove K., Laudet V., Maina C.v.;
Phirofilaria immitis encodes dinhr-7, a putative homolog
Drosophila ecdysone-regulated E78 gene. ",
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS
EMBL; AF367207; AAK54128.1; -.
InterPro; IPR001536; Hormone_rec_lig.
InterPro; IPR001628; Znf_C4steroid.
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Q967S2;
Q1-DEC-2001
Q1-DEC-2001
Q1-JUN-2002
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Q9CK00;
01-JUN-2001
01-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dirofilaria immitis
Eukaryota: Metazoa;
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Pasteurella
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Onchocercidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NHR-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nuclear receptor nhr-7B.
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166 WLVWIS
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(TrEMBLrel. 17, 1
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d protein PM1838.
  171
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                                                                                          Conservative
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83.3%;
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h; Chromadorea;
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l; Mismatches (
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0B31A94DD2AAA2F9 CRC64;
                                                                                                                                                                                 2C01ED1D96C86C9E CRC64;
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RESULT
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Q8Y0V2
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Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
Chandler M., Cholsne N., Claudel-Renard C., Cunnac S., Demange N.,
Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
Siguier P., Thebault P., Whalen M., Wincker P., Levy M.,
Meissenbach J., Boucher C.A.;
"Genome sequence of the plant pathogen Ralstonia solanacearum.";
"Nature 415:497-502(202).
In RemBL; AL646061; CAD14643.1; -.
InterPro; IPR001915; Peptidase_M48.
InterPro; IPR001915; Peptidase_M48.
Pfam; PF01435; Peptidase_M48.
Q SEQUENCE 418 AA; 46610 MW; BACCDD9903C85D52 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
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                                           pfam; pF00104; hormone_rec; 1.
pfam; pF00105; zf-c4; 1.
proDom; pD000035; zf-c4; 1.
proSITE; pS00031; NUCLEAR_RECEPTOR; UNKNOWN_1.
                                                                                                 Crossgrove K., Laudet V., Maina C.V.;

"Dirofilaria immitis encodes dinhr-7, a putative homolog of the Drosophila ecdysone-regulated E78 gene.";

Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.

-! SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

-! SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.

EMBL; AF367208; AAK54129.1;

InterPro; IPR000536; Hormone_rec_lig.

InterPro; IPR001528; Znf_4steroid.
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01-DEC-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
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01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last amoutation update)
   SEQUENCE
                                                                                                                                                                                                                                                                                    Dirofilaria immitis (Canine heartworm).
Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
Onchocercidae; Dirofilaria.
                                                                                                                                                                                                                                                                                                                                                                                                                         Q967S1
                             DNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                Nuclear receptor nhr-7C
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Bacteria; Proteobacteria;
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               linc-finger
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                                                                                                                                                                                                                                                                      NCBI_TaxID-6287;
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 ĀΑ;
   52253 MW;
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83.3%;
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ia; beta subdivision; Ralsto
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21,
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Last sequence update)
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Pred. No.
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                              Receptor;
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 A3430D0FAC35DF8E CRC64
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                             Transcription regulation,
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es 0;
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RESULT 12
Q9L4I1
     RESULT
Q8Z9F2
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Best Local
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Q8Z9F2;
01-MAR-2002 (TrEMBLrel. 2
01-MAR-2002 (TrEMBLrel. 2
01-JUN-2002 (TrEMBLrel. 2
                                                                                                                                                                                                                                Q9L4I1 PRELIMINARY; PRT; 468 AA.
Q9L4I1;
Q1-QCT-2000 (TrEMBLrel. 15, Created)
Q1-QCT-2000 (TrEMBLrel. 15, Last sequence update)
Q1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 52.4 kDa protein (Putative permease of Na+:galactoside symporter family).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M. Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hanlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
  Cano D., Casadesus J., "Characterization of a
                                             STRAIN-SL1344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001092; HLH_basic.
InterPro; IPR001927; Na/Gal_symp.
TIGREAMS; TIGR00792; pgb; 1.
PROSITE; PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.
Hypothetical protein; Complete proteome.
Hypothetical protein; Complete Proteome.
Hypothetical protein; Complete Proteome.
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Nature 413:848-852(2001)
EMBL: AL627265; CAD01308.1;
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                                                                         SEQUENCE FROM N.A.
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83.3%;
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83.3%;
Garcia-del Portillo
Salmonella-specific
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20,
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3.3e+02;
F.; region located between
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RESULT 14
Q9U6X2
ID Q9U6X
AC Q9U6X
DT 01-MP
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Q19337
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                                                                                                                                                                     "Genome sequence";
investigating biology.";
Science 282:2012-2018(1998).
Science 282:2012-2018(1998).
EMBL; Z68297; CAA92595.1; ...
Q9U6X2;
Q9U6X2;
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                           Q19337
Q19337;
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EMBL; AJ242516; CAB89838.1; -.

EMBL; AB008700; AAL19113.1; -.

InterPro; IPR001092; HLH_basic.

InterPro; IPR001927; Na/Gal_symp.

TIGRFAMs; TIGR00792; gph; 1.

PROSITE; PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.

Hypothetical protein; Complete proteome.

SEQUENCE 468 AA; 52443 MW; 5545B43CB3EA0B3A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1996 (TrEMBLrel. 01, 01-JAN-1998 (TrEMBLrel. 05, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-LT2 / SGSC1412 / ATCC 700720;
MEDLINE-21534948; PubMed-11677609;
McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
Waterston R., Wilson R.K.;
                                                                                                                                                                                                                                        none;
                                                                                                                                                                                                                                                    MEDLINE=99069613;
                                                                                                                                                                                                                                                                                       Submitted
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                                                                                                                                                                                                                                                                                                              SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                            Caenorhabditis elegans
Eukaryota; Metazoa; Ner
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                                                                                                                                                                                                                                                                                                                                                                                          Fīla10.5 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and aroP genes."; Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                 Rhabditidae; Peloderinae;
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                                                                                                                                                                                                                            "Genome sequence of the nematode
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                                                                                                                                Local Similarity tes 5; Conserv
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                        PRELIMINARY;
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83.3%;
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83.3%;
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Pred. No. 3.3e
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Pred. No.
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3.3e+02;
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RESULT
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Best Local
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Q967S3;
01-DEC-2001 (TrEMBLrel. 1
01-DEC-2001 (TrEMBLrel. 1
01-JUN-2002 (TrEMBLrel. 2
Nuclear receptor nhr-7A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      volvulus.";
Mol. Bioche
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MO1. Biochem. Parasitol. 104:259-269(1999).
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY EMBL; AF170551; AAF06997.1; -.
HSSP; P20393; 1A6Y.
                                  pfam; PF00104; hormone_rec; 1.
pfam; PF00105; zf-c4; 1.
probom; PD000035; zf-c4; 1.
prosom; PD000031; NUCLEAR_RECEPTOR; UNKNOWN_1
prosite; PS00031; NUCLEAR_RECEPTOR;
                                                                                                                                    Drosophila ecdysone-regulated E78 gene.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
                                                                                                                                                                           Crossgrove K., Laudet V., Maina C.V., "Dirofilaria immitis encodes dinhr-7,
                                                                                                                                                                                                                           Onchocercidae; I
NCBI_TaxID=6287;
                                                                                                                                                                                                                                                       Eukaryota;
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SMART; SM00399; ZnF_C4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00398; STRDHORMONER.
PRINTS; PR00047; STROIDFINGER.
ProDom; PD000035; Znf_C4steroid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unnasch T.R., Bradley J., Beauchamp J., "Characterization of a putative nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Onchocerca volvulus.
Eukaryota, Metazoa; Nematoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                    InterPro; IPR000536; Hormone_rec_lig.
InterPro; IPR001628; Znf_C4steroid.
                                                                                                             -!- SUBCELLULAR LOCATION: NUCLEAR (BY 6-!- SIMILARITY: BELONGS TO THE NUCLEAR EMBL; AF367206; AAK54127.1; --
                                                                                                                                                                                                                                                                   Dirofilaria
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MEDLINE=20058753; PubMed=10593180;
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          Zinc-finger
                      DNA-binding; Nuclear protein;
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                                                                                                                                                                                                                                                                                NHR-7
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IPR001723; Stdhrmn_receptor.
IPR001628; Znf_C4steroid.
556
                                                                                                                                                                                                                                                       Metazoa;
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AA;
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63342
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83.3%;
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19,
21,
MW;
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Pred. No.
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                      Receptor;
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2F7995FAFEB5126F CRC64
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                       Transcription regulation;
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from Onchocerca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                     Filarioidea;
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                                                                                                                           FAMILY
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Minimum
Maximum
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Listing first 45 s
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      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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80
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seq length: 2000000000
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1: /cgn2_6/ptodata/1,
2: /cgn2_6/ptodata/1,
3: /cgn2_6/ptodata/1,
4: /cgn2_6/ptodata/1,
5: /cgn2_6/ptodata/1,
6: /cgn2_6/ptodata/1,
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38
1 WLVWIA 6
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Gapop 10.0 ,
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      /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
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/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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 5200183-5
US-08-469-260A-478
US-08-137-117D-35
US-08-137-117D-35
5223610-5
5223610-5
52344657-5
5433945-5
US-09-122-1268-2
US-09-1316-080-5
US-09-316-080-2
US-09-316-080-2
US-08-653-365A-19
US-08-663-566A-19
US-08-663-56A-19
US-08-663-56A-19
US-08-663-56A-19
US-08-663-56A-19
US-08-653-56A-19
US-08-653-56A-19
US-08-653-56A-15
US-08-653-56A-15
US-08-653-56A-15
US-08-653-56A-15
US-08-62-240A-15
US-08-63-240A-15
US-08-710-48-28
US-08-710-48-28
US-08-710-48-28
US-08-710-828-2
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PCT-US93-08528-16
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(without alignments)
19.615 Million cell updates/sec
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                                                                                                                                                                                                                Sequence 478, Appl
Sequence 35, Appl
Sequence 35, Appl
Sequence 35, Appl
Patent No. 5234657
Patent No. 5244657
Patent No. 5433945
Sequence 2, Appli
Sequence 534, App
Sequence 5, Appli
Sequence 2, Appli
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Sequence
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2, Appli
2, Appli
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19, Appl
19, Appl
19, Appl
19, Appl
15, Appl
17, Appl
18, Appl
19, Appl
19, Appl
11, Appl
11, Appl
12, Appl
13, Appl
15,                                                                                                                                                                                                                                                                                                                                                                      16, Appl
16, Appl
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WLVWI 5

Query Mata Best Loca Matches	RESULT 1 US-08-118-270-16 US-08-118-270-16 Sequence 16, Application U Patent No. 550384 GENERAL INFORMATION: APPLICANT: Murphy, Ran APPLICANT: Schuster, D TITLE OF INVENTION: PATENT OF SEQUENCES: ADDRESSE: BROWDY AN STREET: 419 Seventh CITY: Washington STATE: D.C. COUNTRY: USA ZIP: 20004 COMPUTER: EIMP PC COM OPERATION TYPE: Ploppy COMPUTER: IBM PC COM OPERATION CATION NUMBER: FILING DATE: 09-SEP- PRIOR APPLICATION UNMBER: FILING DATE: 10-SEP- PRIOR APPLICATION UNMBER: APPLICATION NUMBER: APPLICATION NUMBER: RESISTRATION NUMBER: REFILEFAX: 202-737-352 TELEFAX: 202-737-352 TELEX: 48633 INFORMATION EOR SEO ID NO SEQUENCE CHARACTERISTIC. LENGTH: 362 amino ac TYPE: amino acid STRANDENESS: Single STREUGLETYPE: peptide US-08-118-270-16	44444333333228 4444433376 4442109876
ch l Similarity 4; Conserva	LT 1 8-118-270-16 8-118-270-16 8-118-270-16 8-118-270-16 8-118-270-16 8-118-270-16 8-118-270-16 8-118-270-16 8-118-270-16 8-118-270-16 8-118-270-16 8-118-270-16 8-118-270-16 8-118-270-16 8-118-270-16	30 78 9 30 78 9
86.8%; y 80.0%; rvative :	dall dall EXPERIENCE E	1143 3 2 4 4 4 4 4 5 5 5 5 5 6 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7
Score 33; DF Pred. No. 3.7	0 AND NDS .0, .27C	US-08-776-949-2 US-08-482-810-2 US-09-027-955-2 US-09-636-805-2 US-09-636-8128-2 US-08-470-419-4 US-08-776-949-4 US-08-482-810-4 US-09-636-805-4 US-09-636-805-4 US-09-636-805-4 US-09-636-805-4 US-09-363-574-11
3 1; Len 7e+02; 3 0;	G-COUPLED PROTE COMPOSITIONS AND Suite 300 Version #1.25	15
gth 362; Indels 0;	METHODS	Sequence
Gaps 0;	THEREOF	e 2, Appli e 4, Appli e 1, Appli e 11, Appl e 69, Appl

D

120 WLVWV 124

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APPLICATION NUMBER: US/08/53
FILING DATE: 12-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 504,635
FILING DATE: 04-APR-1990
APPLICATION NUMBER: 122,410
FILING DATE: 19-NOV-1987
SEQ ID NO:5:
                                                                                                                                                                                                                                                                                          RESULT 3
5200183-5
5200183-5
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; MOLECULE TYPE:
PCT-US93-08528-16
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                                                                                                                                                                                                                                                                       Patent No. 5200183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 16, Application PC/TUS9308528
GENERAL INFORMATION:
APPLICANT: New York University
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 248633
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                       APPLICANT: TANG, JORDAN J.N.; WAN
TITLE OF INVENTION: RECOMBINANT
NUMBER OF SEQUENCES: 22
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 362 amino acids
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TELEFAX: 202-737-3528
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APPLICATION NUMBER: PC'
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MEDIUM TYPE: Floppy disk
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: si
                  LENGTH: 572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY-2 PCT
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419 Seventh Street, N.W., Suite 300
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linear
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Pred. No. 3.7e+02;
1; Mismatches 0;
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US-08-469-260A-478
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                                                           Query Match
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Matches 4
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Best Local Similarity 80.4
Matches 4; Conservative
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                                                                                                                                                                                                                       TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: POREMBSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5527
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC-COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: I
FILING DATE:
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ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: JAMES C. ERKER
APPLICANT: SHERI L. BUIJK
APPLICANT: ISA K. MUSHAHMAR
APPLICANT: ISA K. MUSHAHMAR
TITLE OF INVENTION: NON-A, NON-B. NON-C, NON-D, NON-E HEPATITIS
TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
NUMBER OF SEQUENCES: 716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: APPLICANT:
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                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/469,260A FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 100 ABBOT
CITY: ABBOTT PARK
STATE: IL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: ABBOTT PARK ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 60064-3500
                                                                           Local Similarity
                                                                                                                                                        TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                      LENGTH:
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2 WLTWLA
                             1 WLVWIA 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOHN N. SIMONS
TAMI J. PILOT-MATIAS
GEORGE J. DAWSON
GEORGE G. SCHLAUDER
SURESH M. DESAI
THOMAS P. LEARY
LEARY
                                                                                                                                                                                      75 amino acids
   7
                                                              Conservative
                                                                           84.2%;
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Pred. No. 5.8e+02;
1; Mismatches (
                                                                           Score 32; DB 4;
Pred. No. 1.2e+02
                                                                         .2e+02;
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                                                                                        Length 75;
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RESULT 5 US-08-137-117D-35

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US-08-436-717-35
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Best Local S
Matches 4
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                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 5340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEF X: 904136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
APPLICANT: BENDIG, Mary
APPLICANT: JONES, Steven
APPLICANT: SALDANHA, JOSE
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 20-DEC-199
                                                                                   APPLICANT: TSUCHIYA, Masayuki
APPLICANT: SATO, Koh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: JP 3-95476 FILING DATE: 25-APR-1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 19-FEB-PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: JP 4-
FILING DATE: 19-FEB-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 3000 K STREET: Washington
                                                                                                                                                                                                                                             52 WIVWI 56
                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
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                                                                                                                                                                                                                                                                           1 WLVWI 5
                                                                                                                                        5, Application US/08436717 5817790
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5795965
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JONES, Steven
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                                                                                                                                                                                                                                                                                                             Conservative
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Pred. No. 2.1e+02;
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                   TO HUMAN
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RESULT 7
5223610-5
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; APPLICANT: Burton, Frank H.;Sutcliffe, Gregor
; --- ^- TNVPNNTION: CHOLERA TOXIN GENE RECULATED
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                                                                                                      5223610-5
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                                                                                                                                    SEQ ID NO:5:
                                             Matches
                                                      Best Local Similarity
                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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ETILING DATE: 19-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 3-9
ETILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO:
                                                                                                                                                              NUMBER OF SEQUENCES: 18
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/137,117
FILING DATE: 20-DEC-1993
APPLICATION NUMBER: WO PCT/JP92/00544
FILING DATE: 24-APR-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: SUCCESTREET: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                  FILING DATE: 18-MAY-1990
) NO:5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/436,717 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0
                                                                                                                                                                                                                                                                                                                               52 WIVWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                    LENGTH: 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
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1 WLVWIA 6
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20007-5109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
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3000 K Street, N.W., Suite
                                             Conservative
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                                                           84.28;
                                                                                                                                                                                                                                                                                                                                                                                                       84.2%;
80.0%;
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                                                      Score 32; I
Pred. No. 3.
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Pred. No. 2.1e+02;
                                             Mismatches
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                                                           .9e+02;
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                                             Indels
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15 WLTWLA

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; Sequence 2, Application US/09122126B
; Patent No. 6431575
; GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: AGGRECAN DEGRADING METALLO PROTEASES
FILE REFERENCE: DM6909
; CURRENT APPLICATION NUMBER: US/09/122,126B
; CURRENT FILING DATE: 1998-07-24
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 2
; LENGTH: 837
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5433945-5
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US-09-122-126B-2
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MUTANTS OF PERTUSSIS TOXIN

NUMBER OF SEQUENCES: 10

CURRENT APPLICATION DATA:

CURRENT APPLICATION UNMBER: US/07/979,798
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Best Local Similarity
Atches 4; Conserve
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; APPLICANT: KLEIN, MICHEL H.;BOUX, HEATHER A.;COCKLE,
;STEPHEN A.;LOOSMORE, SHEENA M.;ZEALEY, GAVIN R.
;TITLE OF INVENTION: IMMUNOPROTECTIVE GENETICALLY-DETOXIFIED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;Patent NO. 5244657
; APPLICANT: KLIEN, MICHEL A.;BOUX, HEATHER A.;COCKLE,
;STEPHEN A.;LOOSMORE, SHEENA M.;ZEALEY, GAVIN R.
; TITLE OF INVENTION: GENETIC DETOXIFICATION OF PERTUSSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID
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Best Local Similarity
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FILING DATE: 20-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 589,423
FILING DATE: 28-SEP-1990
APPLICATION NUMBER: 275,376
FILING DATE: 23-NOV-1988
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APPLICATION NUMBER: US/07/589,423
FILING DATE: 28 SEP-1990
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                             15 WLTWLA 20
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66.7%;
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66.7%;
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Pred. No. 3.9e+02;
1; Mismatches 1
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Pred. No. 3.9e+02;
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US-08-469-260A-534
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                              Query Match
Best Local S
Matches 3
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Matches 4; Conserv
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                                                                                                                                                                                  TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/424,5
EILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: POREMBSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5527.P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: JOHN N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: THOMAS P. LEARY
APPLICANT: ANTHONY SCOTT MUERHOFF
APPLICANT: JAMES C. ERKER
APPLICANT: SHERI L. BUIJK
APPLICANT: SHERI L. BUIJK
APPLICANT: ISA K. MUSHAHWAR
TITLE OF INVENTION: NON-A, NON-B. NON-C, NON-B, NON-E HEPATITIS
TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
NUMBER OF SEQUENCES: 716
                                                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LABORATORIES
                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: 708-937-6365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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                                Local Similarity
les 3; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33 WLVWL 37
                                                                                                                          TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/469,260A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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                                                                                                                                                       LENGTH:
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 1 WLVWIA 6
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: IL
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GEORGE G. SCHLAUDER
SURESH M. DESAI
THOMAS P. LEARY
                                                                                                                                                    50 amino acids
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                                Conservative
                                                                                                          protein
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                                              81.6%;
50.0%;
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                                              Score 31;
Pred. No.
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Pred. No. 1.2e+03;
                                Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                       Version #1.25
                         DB 4; LC
J. 1.1e+02;
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                                                             Length 50;
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                            Gaps
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                                                                                                                                                                         ; SEQ ID NO 2
; LENGTH: 380
; TYPE: PRT
; ORGANISM: Fusarium
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                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:

APPLICANT: John C. Royer

APPLICANT: John C. Christianson

APPLICANT: Gregory A. Gambetta

APPLICANT: Gregory A. Gambetta

APPLICANT: Suzanne M. Otani

APPLICANT: Suzanne M. Otani

APPLICANT: Wendy T. Yoder

TITLE OF INVENTION: Methods For Producing Heterologous

TITLE OF INVENTION: Muthant Cells

TITLE OF INVENTION: Muthant Cells

TITLE OF INVENTION NUMBER: US/09/316,080

CURRENT APPLICATION NUMBER: US/09/316,080

CURRENT FILING DATE: 1999-05-20

EARLIER APPLICATION NUMBER: 09/082,217

EARLIER FILING DATE: 1998-05-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; SEQ ID NO 5
; LENGTH: 377
; TYPE: PRT
; ORGANISM: Fusarium
                                                                          Query Match
Best Local S
Matches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence 2, Application US/09316080 Patent No. 6180366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: John C. Royer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best
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APPLICANT: Wendy T. Yoder
ITTLE OF INVENTION: Methods For Producing Heterologous
ITTLE OF INVENTION: Methods For Producing Heterologous
ITTLE OF INVENTION: Mutant Cells
FILE FILE OF INVENTION: Mutant Cells
FILE REFERENCE: 5563.200-US
CURRENT APPLICATION NUMBER: US/09/316,080
CURRENT FILING DATE: 1999-05-20
EARLIER FILING DATE: 1999-05-20
ARLIER FILING DATE: 1998-05-20
UMMBER OF SEQ ID NOS: 24

NUMBER OF SEQ ID NOS: 24

SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Lynne M. Christianson
APPLICANT: Gregory A. Gambetta
APPLICANT: Howard Brody
                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSEQ for Windows Version 3.0
220 WMVWV 224
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les 3; Conserv
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nes 3; Conserv
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                                                                            Conservative
                                                                                            81.6%;
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                                                                                            Score 31; DB 4;
Pred. No. 7.6e+02;
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Pred. No. 7.5e+02;
                                                                          Mismatches
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                                                                                                               Length 380;
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RESULT 15
US-08-663-566A-19
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Best Local Similarity
Thes 3; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-952-365-2
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US-08-952-365-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Patent No. 6274311
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                              Sequence 19, Application US/08663566A Patent No. 5853733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/08952365 Patent No. 6274311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Kurdydyk, Linda M.
REGISTRATION NUMBER: 34,
                                                                                                                                                                                                                              APPLICANT: Cochran, Mark D
APPLICANT: Macdonald, Richard D
APPLICANT: Macdonald, Richard D
TITLE OF INVENTION: Recombinant Herpesvirus
TITLE OF INVENTION: and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 438 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOTTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                133 WMVWV 137
           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: Canada
ZIP: M5H 3Y2
                                                                                              COUNTRY: U:
ZIP: 10036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Toronto
STATE: Ontario
                                                                                                                                            CITY: New York
                                                                                                                                                             STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
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                                                                                                                                New York
                                                                                                                                                             1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            438 amino acids
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                                                                                                             USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (416)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         361-1398
361-1398
2:
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                                                                                                                                                                                                                            and Uses
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6580-63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 31; DB
Pred. No. 8.70
2; Mismatches
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               Version
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J.7e+02;
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APPLICATION NUMBER: US/08/663,566A
FILING DATE: June 13, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P
REGISTRATION NUMBER: 28,678
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)278-0400
TELERA: (212)278-0260
TELEX: 42523
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CCHARACTERISTICS:
LENGTH: 705 amino acids
TYPE: molecular Type: protein
HYPOTHETICAL: NO
ON-15-16-19
US-08-663-566A-19

81.6%: Score
Search completed: January 3, 2003, 15:34:32 Job time : 10 secs
                                                                         Дb
                                                                                                                                      Nuery Match 81.6%;
Pest Local Similarity 66.7%;
Matches 4; Conservative
                                                                       1 WLVWIA 6
| ||:|
640 WYVWLA 645
                                                                                                                                          Score 31; DB 2; Length 705; Pred. No. 1.4e+03; 1; Mismatches 1; Indels
                                                                                                                                          0;
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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Database
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   Published_Applications_AA:*

1: /cgn2_6/ptodata/1/pubpaa/US

2: /cgn2_6/ptodata/1/pubpaa/US

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11: /cgn2_6/ptodata/1/pubpaa/US
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Gapop 10.0 ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Maximum Match 100%
Listing first 45 summaries
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(without alignments)
23.825 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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٠	1 4 4	441	441	438	401	126	96	86	73	50	837	560	110	75	735	296	420	49	230	Length
u	5	10	10	10	10	10	10	10	10	8	12	10	10	8	10	10	10	10	9	DB
00-03-332-330-1//	12-09-093-508-177	TIC-00-005-606-1	US-09-871-874-21	US-09-894-993-2	US-09-871-874-11	US-09-864-761-48848	US-09-864-761-33793	US-09-864-761-48030	US-09-864-761-37732	US-08-424-550B-534	US-10-052-586-352	US-09-815-242-11746	US-09-867-550-298	US-08-424-550B-478	US-09-815-242-12089	US-09-741-669-378	US-09-815-242-11260	US-09-995-494-75	US-09-738-626-3571	ID
sequence I//, App			21.	Sequence 2, Appli	Sequence 11, Appl	Sequence 48848, A	Sequence 33793, A	Sequence 48030, A	Sequence 37732, A	Sequence 534, App	Sequence 352, App	Sequence 11746, A	Sequence 298, App	Sequence 478, App	Sequence 12089, A	Sequence 378, App	Sequence 11260, A	Sequence 75, Appl	Sequence 3571, Ap	Description

	45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20
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	10	5	10	9	12	12	10	10	10	10	10	10	10	10	10	10	10	10	9	9	9	9	9	9	9	9
ALIGNMENTS	US-09-871-874-9	115-09-951-780-2	US-09-871-874-10	US-09-738-626-6356	US-10-052-586-148	US-10-006-867-32	US-09-989-721-177	-09-990-45	US-09-993-604-177	US-09-991-163-177	US-09-990-442-177	US-09-991-073-177	US-09-989-732-177	US-09-989-731-177	US-09-989-727-177	US-09-989-279-177	US-09-989-723-177	US-09-989-722-177	US-09-993-687-177	US-09-991-181-177	US-09-990-436-177	US-09-989-730-177	US-09-990-444-177	US-09-989-735-177	US-10-063-547-32	US-09-989-293A-177
			e 10,	Sequence 6356, Ap	Sequence 148, App	Sequence 32, Appl	Sequence 177, App	177,	177,	`			177,	Sequence 177, App	177,		Sequence 32, Appl	Sequence 177, App								

RESULT 1
US-09-738-626-3571
Sequence 3571, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: HAYASHI, MIKIRO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: TATEISHI, NAOKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR APPLICATION NUMBER: JP 90/159162
PRIOR APPLICATION NUMBER: JP 90/280988
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SEQ ID NO 3571
LENGTH: 230
TYPE: PRT
ORGANISM: Corynebacterium glutamicum
US-09-738-626-3571

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; TYPE: PRT
; ORGANISM: Homo sapien
US-09-995-494-75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JS-09-815-242-11260
                                                                                                                                PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
                SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 11260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 11260, Application Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn version 3.1 SEQ ID NO 75 LENGTH: 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Chen, Sei-Yu
TITLE OF INVENTION: Compositions and Methods Relating to Prostate Specific Genes
FILE REFERENCE: DEX-0293
CURRENT APPLICATION NUMBER: US/09/995,494
CURRENT FILING DATE: 2001-11-27
PRIOR APPLICATION NUMBER: 60/253,176
PRIOR APPLICATION NUMBER: 60/253,176
PRIOR FILING DATE: 2000-11-27
NUMBER OF SEQ ID NOS: 115
                                                                      PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
                                                          NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Xu, H. Howard
ITTLE OF INVENTION: Identification of Essential Genes in
ITTLE OF INVENTION: Prokaryotes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Salceda, Susana
APPLICANT: Macina, Roberto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Haselbeck, Robert
ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 WVVWVA 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 WLVWIA 6
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Liu, Chenghua
Chen, Sei-Yu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ohlsen, Kari L.
Zyskind, Judith W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Trawick, John D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wall, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cafferkey,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Carr, Grant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ali, Shujath
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yamamoto, Robert T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Application US/09815242
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Query Match
Best Local Similarity
Watches 5; Conserve
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US-09-741-669-378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Escherichia coli
US-09-741-669-378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Haemophilus influenzae US-09-815-242-11260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-815-242-12089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 1999-12-23

NUMBER OF SEQ ID NOS: 481

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 378

LENGTH: 296

TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
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                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 12089, Application US/09815242 Patent No. US20020061569A1
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APPLICANT:
APPLICANT:
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                                                                                                                    TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITER. 011A,
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/206,848
                                PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
                                                                                                                                                                                                                                                                                                       APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/741,669
CURRENT FILING DATE: 2000-12-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Genes identified as required for TITLE OF INVENTION: proliferation of E. coli FILE REFERENCE: ELITRA.009A
                                                                                                                                                                                                                                                                    APPLICANT:
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APPLICATION NUMBER: 60/253,625 FILING DATE: 2000-11-27
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Ohlsen, Kari L.
Zyskind, Judith W.
                                                                                                                                                                                                                                                                 Carr, Grant J.
Yamamoto, Robert T
Xu, H. Howard
                                                                                                                                                                                                                                                                                                                                                      Ohlsen, Kari L.
Zyskind, Judith W.
                                                                                                                                                                                                                                                                                                                       Trawick, John D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 33;
Pred. No.
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95;
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TOPOLOGY: 11;

MOLECULE TYPE:
US-08-424-550B-478
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PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FRATSEQ for Windows Version 4.0
SEQ ID NO 12089
LENGTH: 735
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Best Local Similarity 80.0%;
Matches 4; Conservative
                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: JOHN N
                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 478:
                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
AMME: POREMBSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 75 amino acids
                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LABORATORIES
STREET: 100 ABBOTT PARK ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: JAMES C. ERKER
APPLICANT: SHERI L. BUIJK
APPLICANT: ISA K. MUSHAHWAR
TITLE OF INVENTION: NON-A, NON-B. NON-C, NON-D, NON-E HEPATITIS
TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
NUMBER OF SEQUENCES: 716
                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Reli
CURRENT APPLICATION DATA:
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                                                                                                                               LENGTH:
TYPE: a
                                                                                                                                                                              TELEPHONE: 706 5. TELEPHONE: 708-938-2623
                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION: 435435
                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
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GEORGE J. DAWSON
GEORGE G. SCHLAUDER
SURESH M. DESAI
THOMAS P. LEARY
ANTHONY SCOTT MUERHOFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
 Conservative
                                                                                                           linear
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                                                                                      protein
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Score 32; DB Pred. No. 39; 1; Mismatches
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Pred. No. 2.3e+02;
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                                   DB 8;
                                 Length 75;
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CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/211 078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
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TITLE OF INVENTION: No. US20020082206Alel Polynucleotides
TITLE OF INVENTION: Thereby
FILE REFERENCE: 21402-013 (Cura-313)
CURRENT APPLICATION NUMBER: US/09/867,550
CURRENT FILING DATE: 2001-09-20
CURRENT FILING DATE: 2001-09-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Leach, Martin D.
APPLICANT: Mehraban, Fuad,
APPLICANT: Conley, Pamela
APPLICANT: Law, Debbie
APPLICANT: Topper, James
                                                                                                                                                                                                                                                                                                         APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamotto, Robert T.
APPLICANT: Yu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: USSN 60/208,427 PRIOR FILING DATE: 2000-05-30 NUMBER OF SEQ ID NOS: 2125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version 4.0
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FEATURE:
NAME/KEY: VARIANT
LOCATION: (37)
OTHER INFORMATION: wherein Xaa may be any one of Ser or Pro or Thr or
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ohlsen, Kari L.
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66.7%;
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Pred. No. 55;
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PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FRSESEQ for Windows Version 4.0
SEQ ID NO 11746
LENGTH: 560
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
US-09-815-242-11746
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Patent No. US20020127584A1
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PRIOR APPLICATION NUMBER: 60/059266
PRIOR FILING DATE: 1997-09-18
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Goddard, Audrey
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APPLICATION NUMBER: 60/081838
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APPLICATION NUMBER: 60/082568
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APPLICATION NUMBER: 60/081070
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APPLICATION NUMBER: 60/081195
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APPLICATION NUMBER: 60/068017
FILING DATE: 1997-12-18
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APPLICATION NUMBER: 60/069425
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60/083499 60/083496 NUMBER: 60/083495

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NUMBER: 60/ : 1998-05-15

NUMBER: 1998-05-07 1998-05-07

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60/084643 60/084640 1 NUMBER: 60/1 2: 1998-03-31

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NUMBER:

60/081049

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NUMBER: 60/079786: 1998-03-27

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APPLICATION NUMBER: 60/
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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
PATENTIN Release #1.0.
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                                                                                                                                                                                     TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: prot
                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 50 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: JAMES C. ERKER
APPLICANT: SHERI L. BUJJK
APPLICANT: ISA K. MUSHAHWAR
TITLE OF INVENTION: NON-A, NON-B. NON-C, NON-D, NON-E I
TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: APPLICANT:
                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
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CORRESPONDENCE ADDRESS:
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708-938-2623
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                                                                                1 WLVWIA 6
                                                                                                                                                                                                                                                                                                                         NAME: POREMBSKI, PRESISTRATION NUMBER:
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TAMI J. PILOT-MATIAS
GEORGE J. DAWSON
GEORGE G. SCHLAUDER
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US-09-864-761-37732
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Lis
TO ID NO 37732
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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
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TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
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OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00665
FILING DATE: 2001-01-30
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INFORMATION:
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     Conservative
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N: EXPRESSED IN HBL100, SIGNAL = 0.99

N: EXPRESSED IN LUNG, SIGNAL = 1.2

N: EXPRESSED IN LUNG, SIGNAL = 1.3

N: EXPRESSED IN HELA, SIGNAL = 1.3

N: EXPRESSED IN HELA, SIGNAL = 1.1

N: EXPRESSED IN HELAT, SIGNAL = 1.1

N: EXPRESSED IN PLACENTA, SIGNAL = 1.3

N: EXPRESSED IN BT474, SIGNAL = 1.5

N: EXPRESSED IN BT474, SIGNAL = 1.2

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David K.
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US 09/608,408
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Score 31; DB Pred. No. 54; 1; Mismatches
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US-09-864-761-48030
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LENGTH: 86
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PRIOR EILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR PTITNG DATE: 2001-01-30
                                                                                                                                                                                                                                                                                        SOFTWARE: Annomax
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PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
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                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 09/774,203 PRIOR FILING DATE: 2001-01-29
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PRIOR APPLICATION NUMBER: PCT/US01/00670
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PRIOR APPLICATION NUMBER: US 60/207,456
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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
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PRIOR APPLICATION NUMBER: US 09/632,366
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT.
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T: Chen, Wensheng
T: Chen, Wensheng
INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
Similarity 4; Conserv
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l, David K.
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                                                                                        MAP TO AL009182.12

EXPRESSED IN LUNG, SIGNAL = 1.2

EXPRESSED IN HELA, SIGNAL = 1.4

EST_HUMAN HIT: BE398021.1, EVALUE 2.00

SMISSPROT HIT: P05882, EVALUE 5.20e-01
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Score 31; DB Pred. No. 63; 1; Mismatches
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NUMBER OF SEQ ID NOS: 49117
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                                                                                                                                                                                                            TYPE: PRT
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OTHER INFORMATION: MAP
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APPLICATION NUMBER: US 60/236,359
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              IN HEART, SIGNAL = 2.3

N ADULT LIVER, SIGNAL = 1

N HELA, SIGNAL = 2.9

IN LUNG, SIGNAL = 1.6

IN FETAL LIVER, SIGNAL = 1

N PLACENTA, SIGNAL = 1

N BRAIN, SIGNAL = 1.1
 BRAIN,
HBL100,
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SIGNAL
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; OTHER INFORMATION: SWISSPROT
; OTHER INFORMATION: EST_HUMAN
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US-09-864-761-33793
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                                                                                                                                                         PRIOR APPLICATION NUMBER: US PRIOR FILING DATE: 2001-01-29 NUMBER OF SEQ ID NOS: 49117
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PRIOR APPLICATION NUMBER: PCT/US01/00663
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
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PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
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PRIOR APPLICATION NUMBER: US 60/236,359
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PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
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                                                                                       TYPE: PI
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FEATURE:
OTHER INFORMATION: MAP TO AC010368.2
OTHER INFORMATION: EXPRESSED IN PLACENTA,
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                                                              ORGANISM: Homo sapiens
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Hanzel, David K.
Chen, Wensheng
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HIT: AU119728.1, EVALUE 1.00e-38
HIT: BE069876.1, EVALUE 8.00e-03
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RESULT 15
US-09-871-874-11
Sequence 11, Application US/09871874
Patent No. US20020081655A1
GENERAL INFORMATION:
APPLICANT: SAVITZKY, Kinneret
APPLICANT: TOPORIK, Amir
TITLE OF INVENTION: Splice Variant of mGlur
TITLE OF INVENTION: Splice Variant of mGlur
FILE REFERENCE: 2786-0176P
CURRENT APPLICATION NUMBER: US/09/871,874
CURRENT FILING DATE: 2001-09-04
NUMBER OF SEQ ID NOS: 21
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 11
LENGTH: 401
TYPE: PRT
ORGANISM: Homo sapiens
US-09-871-874-11
Search completed: January 3, 2003, 15:52:07 Job time: 4.77273 secs
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                                                                                                                                                                Query Match 81.6%; Score 31; DB 10; Length 401; Best Local Similarity 80.0%; Pred. No. 2.6e+02; Matches 4; Conservative 1; Mismatches 0; Indels
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Result
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Maximum Match 100%
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Match Length DB
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 GenCore version 5.1.3 (c) 1993 - 2003 Compugen Ltd
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57.944 Million cell updates/sec
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ALIGNMENTS

R; Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kon, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: B87530
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-101 <STO> A;Molecule type: DNA
A;Residues: 1-35 <REA>
A;Residues: -35 <REA>
A;Cross-references: GB:AE002165; GB:AE002161; NID:g7188948; PIDN:AAF37906.1; PID:g718
A;Experimental source: strain AR39, HL cells
C;Genetics:
C;Genet CP0010 A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39 A;Reference number: A81500; MUID:20150255; PMID:10684935 A;Accession: D81522 R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O., C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Nucleic Acids Res. 28, 1397-1406, 2000 hypothetical protein CP0010 [imported] - Chlamydophila pneumoniae (strain AR39) C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 11-May-2000 C;Accession: D81622 Q C; Genetics: A; Gene: CC2267 hypothetical protein CC2267 [imported] - Caulobacter crescentus c;Species: Caulobacter crescentus C;Species: Caulobacter crescentus C;Date: 20-Apr-2001 *sequence_revision 20-Apr-2001 #text_change 20-Apr-2001 C;Accession: B87530 Дb A; Status: preliminary D81622 A;Cross-references: GB:AE005673; NID:g13423780; PIDN:AAK24238.1; GSPDB:GN00148 Query Match Best Local S Matches 5 Matches Query Match Best Local N 6 VFFWLK 11 1 IFFWIK 6 4. Similarity 5; Conser Similarity Conservative 88.9%; 91.7%; 66.7%; 2; Score 32; Pred. No. Score 33; Pred. No. Mismatches DB 13; DB 2 0; Length 35; Length 101; Indels 0; Gaps 0. 0; ; Hicke Salzbe

Conservative

Mismatches

0;

Indels

0,

Gaps

0,

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conserved hypothetical protein MYPU_4610 [imported] - Mycoplasma pulmonis (strain C;Species: Mycoplasma pulmonis·
C;Date: 24-May-2001 #sequencq_revision 24-May-2001 #text_change 03-Aug-2001
C;Accession: E90569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Murray, J.; Wohldmann, P.; Bauer, C.; Biewald, T. submitted to the EMBL Data Library, September 1997 A;Description: The sequence of C. elegans cosmid T03D3 A;Reference number: Z21136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Leblanc, C.; Boyen, C.; Richard, O.; Bonnard, G.; Grienenberger, J.M.; Kloareg, B. J. Mol. Biol. 250, 484-495, 1995
A;Title: Complete sequence of the mitochondrial DNA of the rhodophyte Chondrus crispus A;Reference number: $59078; MUID:95341681; PMID:7616569
A;Accession: $59082
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A; Introns: 17/3;
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C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change
C;Accession: T32207
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Olecule type: DNA
Residues: 1-374 <MUR>
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R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; (Nucleic Acids Res. 29, 2145-2153, 2001
A;Title: The complete genome sequence of the murine respiratory A;Reference number: A99512; MUID:21267165; PMID:11353084
A;Accession: E90569
A; Molecule type: DNA
A; Residues: 1-660 < KUR>
A; Cross-references: GB: AE008687; PIDN: AAL46227.1;
                                                                                                                                          Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001 A; Authors: Yoo, H.; Tao, Y.; Biddle,
                                                     A; Status: preliminary
                                                                    A; Title: The Genome of the Natural Genetic A; Reference number: AB2577; PMID:11743193 A; Accession: AE3226
                                                                                                                             A; Authors: Yoo, H.; Tao, ster, E.W.
                                                                                                                                                                                                R; Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, erage, G.; Gillet, W.; Grant, C.; Guenthner,
                                                                                                                                                                                                                                   conserved hypothetical protein Atu5541 [imported] - Agrobacterium tumefaciens
c;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
C;Accession: AE3226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Date: 28-Jul-2000 *sequence_revision 28-Jul-2000 *text_change C;Accession: T51162
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A;Molecule type: DNA
A;Residues: 1-423 <KUR>
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Mismatches 0;
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 PID:g17744003;
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                                                                                                             tumefaciens C58
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strain C58 (Dupont)

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A;Molecule type: DNA
A;Residues: I-988 <COL>
A;Cross-references: GB:AE001212; GB:AE000520; NID:g3322597; PIDN:AAC65312.1; PID:g332260
A;Experimental source: strain Nichols
C;Genetics:
A;Gene: TP0325
C;Superfamily: syphilis spirochete conserved hypothetical protein TP0325
                                QΥ
                                                                                                                                                     C; Genetics:
A; Gene: STY3003
                                                                                                                                                                                                             A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-86 <PAR>
                                                                                                                                                                                                                                                                               R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica sero; A;Reference number: AB0502; PMID:11677608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     conserved hypothetical protein TP0325 - syphilis spirochete C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete) C:Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 21-Jan-2000 C:Accession: H71338
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                                                                                                                                                                                       A;Cross-references: GB:AL513382; PIDN:CAD05987.1; PID:g16503958; GSPDB:GN00176
                                                                                                                                                                                                                                                                     A; Reference number: A; Accession: AD0850
                                                                                                                                                                                                                                                                                                                                                                                                                                           doubtful CDS found within S. typhi pathogenicity island [imported] - Salmonella Species: Salmonella enterica subsp. enterica serovar Typhi pte: this species has also been called Salmonella typhi pate: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete A;Reference number: A71250; MUID:98332770; PMID:9665876 A;Accession: H71338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Genome: plasmid
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A;Gene: Atu5541
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ey, L.; Weidman, J.; Smit
ience 281, 375-388, 1998
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53 LFYWIK 58
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66.7%;
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47;
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A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing arch A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: D69381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Fulton, R.; Hawkins, J.; Rohlfing, T. submitted to the EMBL Data Library, October 1998 A;Description: The sequence of C. elegans cosmid F43B10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary; nucleic acid sequence not shown; translation A;Molecule type: DNA A;Residues: 1-162 <KLE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dod; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E. Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Nature 390, 364-370, 1997
                                             R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, I
                                                                                                                      A;Note: Nostoc sp. strain PCC 7120 is a synonym of C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Map position:
A; Introns: 88/2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein F43B10.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 04-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
                        DNA Res. 8, 205-213,
                                                                                                 C; Accession: AG2542
                                                                                                                                                                         hypothetical protein all7626 [imported] - Nostoc sp. (strain PCC 7120) plasmid C; Species: Nostoc sp.
                                                                                                                                                                                                                                                             RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Experimental source:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; translated from GB/EMBL/DDBJ
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;Introns: 88/2; 103/3; 128/3
;Superfamily: Caenorhabditis elegans hypothetical protein F43B10.1
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100.0%; pr
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Sequence of the Filamentous Nitrogen-fixing Cyanobacterium
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Pred. No. 1.3e+
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIDN:AAC67400.1; GSPDB:GN00028; CESP:F43B10.1 tol N2; clone F43B10
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                                                                                                                         Anabaena sp. strain PCC #text_change 30-Jun-2002
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                                                   Yasuda, M.;
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A;Cross-references: GB:AE001802; GB:AE000512; NID:g4982133; PIDN:AAD36643.1; PID:g498214
A:Experimental source: strain MSB8
C:Genetics:
                                                                                                                                                                                                                A;Reference number: A72200; MUID:99287316; PMID:10360571 A;Accession: A72238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C:Species: Synechocystis sp.
A:Variety: PCC 6803
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
C:Accession: S75891
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.: Nakamura, V. P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: al
A;Genome:
                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-267 < ARN>
                                                                                                                                                                                                                                                                                                                                                  hemolysin - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: A72238
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Best Local Similarity
Thes 5; Conserv
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A;Cross-references: EMBL:D90913; GB:AB001339; NID:g1653348; PIDN:BAA18350.1;
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Accession: $75891
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Nakamura, and the second of the unicellular cyanobacte. A;Title: Sequence analysis of the genome of the unicellular cyanobacte.
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A;Reference number: S74322; MUID:97061201; PMID:8905231
A;Accession: S75891
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                                                                                                                                                                                                   A; Status: preliminary
                                                                                                                                                                                                                                                                             Nature 399, 323-329, 1999
                                                                                                                                                                                                                                                                                                            R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hi
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
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A;Accession: AG2542
A;Status: preliminary
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hypothetical protein F1C12.211 - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 23-Jul-1999 C:Accession: T05338 R:Bevan, M.; Terryn, N.; Ardiles, W.; Buysshaert, C.; Dasseville, R.; De Cleewes, H.W.; Mayer, K.F.X.; Schueller, C. submitted to the Protein Sequence Database, April 1998 A;Reference number: Z15408 A;Accession: T05338
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A; Introns: 37/2; 116/2;
A; Note: F1C12.211
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A;Cross-references: EMBL:AL022224
A;Cross-references: EMBL:AL022224
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Search completed: January Job time: 10.9545 secs
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Query Match
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           Chloroplast.
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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                                                                                                                                                   Q9MUL1;
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Nature 390:364-370(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=VC-16 / DSM 4304 / ATCC 49
MEDLINE=98049343; PubMed=9389475;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales; Archaeoglobaceae; Archaeoglobus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Archaeoglobus fulgidus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein AF1052 precursor
                                                                                                                                                                                                                                                    68 VYFWVK 73
                                                                                                                                                                                                                                                                                                                  Local Similarity les 3; Conserv
                                                                                                                                                                                                                                                                                   1 IFFWIK 6
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162 AA;
                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
Mesostigmataceae;
                                                                                                                                                                                                                                                                                                                                                                                                 162
                                                                                                                                                                                                                                                                                                                                                                                   18043 MW;
                                                                                                                                                                                                                                                                                                                                   86.1%;
             Streptophyta; Mesostigmatophyceae;
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••
                                                                                                                                                                                                                                                                                                                                Score 31;
Pred. No.
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Mesostigma
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NORB_PSEST
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Best Local
EPR SPECTROSCOPY.

EPR SPECTROSCOPY.

STRAIN-ATCC 14405 / Zobell;

MEDLINE-98191362; PubMed-9521721;

Cheesman M.R., Zumft W.G., Thomso
                                                                                                                                                                                                                                                                                                                                                                      Zumft W.G., Braun C., Cuypers H.;
Zumft W.G., Braun C., Cuypers H.;
"Nitric oxide reductase from Pseudomonas stutzeri. Primary structure
and gene organization of a novel bacterial cytochrome bc complex.";
Eur. J. Biochem. 219:481-490(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P98008:
01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Nitric-oxide reductase subunit B (EC 1.7.99.7)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-94139726;
Zumft w c
                                                                                                                                                                                               cytochrome
                                                                                                                                                                                                                                                                                                       EPR SPECTROSCOPY.
STRAIN-ATCC 14405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pseudomonas stutzeri (Pseudomonas perfectomarina)
Bacteria; Proteobacteria; gamma subdivision; Pseud
                                                                                                                                              J. Bacteriol.
                                                                                                                                                                                                                             "Formation
                                                                                                                                                                                                                                                      Heiss B.
                                                                                                                                                                                                                                                                            MEDLINE-89255095;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pseudomonas
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PROSITE; PS00668; COMPLEX1_ND1_2; 1.
OXIDOREDUCTASE; NAD; Plaststoquinone; Chloroplast; Transf
SEQUENCE 367 AA; 40369 MW; 158CF9E44A58EB98 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF166114; AAF43887.1; -. InterPro; IPR001694; Resp_NADH_dh1. Pfam; PF00146; NADHdh; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               branch of green plant evolution.";
Nature 403:649-652(2000).
-i- CATALYTIC ACTIVITY: NADH + plastoquinone = NAD(+) + plastoquinol.
-i- SIMILARITY: BELLONGS TO THE COMPLEX I SUBUNIT 1 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=316;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lemieux C., Otis C., Turmel M.;
"Ancestral chloroplast genome in Mesostigma viride reveals an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=20150907; PubMed=10688199;
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5; Conserv
                                                                                                                                                                                                                     9255095; PubMed=2542222;
Frunzke K., Zumft W.G.;
on of the N-N bond from nitric oxide by
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                                                                                                                                                                                         complex of nitrate-respiring
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100.0%;
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Pred. No. 85;
Mismatches
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Thomson A.J.;

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NU4M_MARPO
ID NU4M_M
AC P26848
DT 01-FEB
DT 01-FEB
DT N14FEB
DE NADH-U
GN MATCHA
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Best Local
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01-FEB-1994
01-FEB-1996
                                             U1-FEB-1996 (Rel. 33, Last annotation update)
NADH-U1-FEB-1996 (Rel. 33, Last annotation update)
NADH-U1-FEB-1996 (Rel. 33, Last annotation update)
                                                                                                                                                                                                                                                                                    TRANSMEM
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               Mitochondrion
                         Marchantia polymorpha
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          structurally related to the heme-copper oxidases."; Biochemistry 37:3994-4000(1998).
-!- FUNCTION: COMPONENT OF THE ANAEROBIC RESPIRATOR
  Eukaryota; Viridiplantae;
                                       ND4 OR NAD4.
                                                                                                   P26848;
                                                                                                             NU4M_MARPO
                                                                                                                                                                                                                                                                        SEQUENCE
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(Rel.
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66.7%;
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                         (Liverwort).
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 Streptophyta; Embryophyta; Marchantiophyta;
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Pred. No.
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(HIGH-SPIN HEME) (PROBABLE).
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NU4M_ACACA
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Q37375;
15-JUL-1998
                                        castellanii: complete sequence,
organization.";
J. Mol. Biol. 245:522-537(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001750; Oxidored_q1. Pfam; PF00361; Oxidored_q1; 1. PRINTS; PR01437; NUOXDRDTASE4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NADH dehydrogenase, nad5, nad4, nad2, in Marchantia polymorpha. Mol. Gen. Genet. 237:343-350(1993).
-i- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oda K., Yamato K., Ohta E., Nakamura Y., Takemura M., Nozato N., Akashi K., Kanegae T., Ogura Y., Kohchi T., Ohyama K.; "Gene organization deduced from the complete sequence of liverwort Marchantia polymorpha mitochondrial DNA. A primitive form of plant mitochondrial genome."; J., Mol. Biol. 223:1-7(1992).
This SWISS-PROT entry is copyright.
                                                                                 Burger G., Plante I., Lonergan K.M., Gray M.W.; "The mitochondrial DNA of the amoeboid protozoo
                                                                                                                          STRAIN-ATCC
                                                                                                                                                                  Eukaryota; Acanthamoebidae;
NCBI_TaxID=5755;
                                                                                                                                                                                                                           ND4 OR NAD4
                                                                                                                                                                                                                                         NADH-ubiquinone
                                                                                                                                                                                                                                                    15-JUL-1998 (Rel. 30-MAY-2000 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oxidoreductase; NA:
SEQUENCE 495 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. Thuse by non-profit institutions as long
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                             -!- CATALYTIC
                                                                                                               MEDLINE=95147275;
                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                Mitochondrion.
                                                                                                                                                                                                            Acanthamoeba castellanii (Amoeba).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   modified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=93247547; PubMed=8483448;
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Oda K., Yamato K., Ohta E., Nakam
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rPro; IPR003918; NADHub_oxred4
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                        245:522-537(1995).
ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
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36, Last sequence update)
39, Last annotation update)
39, Last annotation update)
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PubMed=7844823;
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56311 MW; 01
                                                                                                                                                                                                                                                                                                                                                                                                                                                      86.1%;
66.7%;
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                                                                                                                                                                                  Acanthamoeba
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0F75894D6CAAAED4 CRC64;
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produced through a collaboration
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                                                              MEDLINE-88280759; PubMed-3200777., MIShihara M., Winters C.A., Buzko E., Mishihara M., Winters C.A., Buzko E., Mormonal regulation of rat Leydig ce
                                                                                                                                                                                                                                 STRAIN-Sprague-Dawley;

MEDLINE-95217329; PubMed=7702752;

Givens C.R., Zhang P., Bair S.R., Mellon S.H.;

Givens C.R., Zhang P., Bair S.R., Mellon S.H.;

"Transcriptional regulation of rat cytochrome P450c17 expression in mouse Leydig MA-10 and adrenal Y-1 cells: identification of a single protein that mediates both basal and cAMP-induced activities.";

DNA Cell Biol. 13:1087-1098(1994).
                                                levels
cDNA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-89076306; PubMed-3264499;
Namiki M., Kitamura M., Buczko E., Dufau M.L.;
"Rat testis P-450(17)alpha cDNA: the deduced amino expression and secondary structural configuration."
Biochem. Biophys. Res. Commun. 157:705-712(1988).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cDNA encoding a unique steroid hydroxylase capable of catalyzing delta 4- and delta 5-steroid-17,20-lyase reactions."; mol. Endocrinol. 3:968-975(1989).
                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Testis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Rat).
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01-AUG-1990 (Rel. 15, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
Cytochrome P450 17 (EC 1.14.99.9) (CYPXVII) (P450-C17) (Steroid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CPT7_RAT
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Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
SEQUENCE 497 AA; 57768 MW; 9C0B637E65C0E3B5 CRC64;
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InterPro; IPR001750; Oxidored_q1.
Pfam; PF00361; oxidored_q1; 1.
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| IFFWI 57
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5; Conser
                   Biophys.
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Bioinformatics Institute. There are no restrictions
proofit institutions as long as its content is in
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Pred. No.
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                         154:151-158(1988)
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                                                                          partial length
                                                                                                      E., Waterman M.R., Dufau M.L.; cell cytochrome P-45017 alpha
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1.1e+02;
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DC Uridin
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Matches 4
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EMBL; X69816; CAA49470.1; -.
EMBL; M31681; AAA41777.1; -.
EMBL; M22204; AAA41783.1; -.
EMBL; M21208; AAA41783.1; -.
EMBL; M27282; AAA41779.1; -.
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P38196;
01-OCT-1994
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Mellon S.H., Vaisse C.;
"CAMP regulates P450scc gene expression by
"CAMP regulates P450scc gene expression by
                                                                                                                                                                                                                                                   Uridine permease.
FUI1 OR YBL042C OR YBL0406.
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      MEDLINE-95176707; PubMed-7871888;
                                      STRAIN=S288c
                                                                SEQUENCE FROM
                                                                                                                                                         Saccharomycetales;
                                                                                                                                                                                      Eukaryota; Fungi;
                                                                                                                                                                                                                      Saccharomyces cerevisiae (Baker's yeast);
                                                                                                                                                                                                                                                                                                             01-OCT-1994 (Rel.
01-OCT-1994 (Rel.
16-OCT-2001 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001128; Cytochrome_P450.
Pfam; PF00067; p450; 1.
PRINTS; PR00385; P450.
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MEDLINE=90046678;
                                                                                                                         NCBI_TaxID=4932;
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FUNCTION: CONVERSION OF PREGNENOLONE AND PROGESTERONE TO THE FUNCTION. TO THE FUNCTION TO THE TOTAL TOTAL THE TOTAL TOTAL THE TOTAL TOTAL THE TOTAL 
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European Bioinformatics Institute. The
by non-profit institutions as long
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PubMed=2554289;
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A535600F7E6A399B CRC64;
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SEQUENCE
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001248; Cyt_pur_permease.
Pfam; PF02133; Transp_cyt_pur; 1.
TIGRFAMS; TIGR00800; ncs1; 1.
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Wagner R., de Montigny J., de Wergifosse P.,
"The ORF YBL042 of Saccharomyces cerevisiae
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beta-galactosidase)
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                                            01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Galactocerebrosidase precursor (EC 3.2.1.46)
                                                                                                 GALC_HUMAN P54803;
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Pfam; PF02057;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long modified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genomics 33:457-462(1996).
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                      (Galactocerebroside beta-galactosidase)
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LEUKODYSTROPHY (GLD). THIS DEFICIENCY RESULTS IN THE IN:
CATABOLISM OF SEVERAL GALACTOLIPIDS THAT ARE IMPORTANT I
PRODUCTION OF NORMAL MYELIN.

SIMILARITY: BELONGS TO FAMILY 59 OF GLYCOSYL HYDROLASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INTESTINE AND COLON (BY SIMILARITY).

CATALYTIC ACTIVITY: D-galactosyl-N-acylsphingosine + H(2)0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       galactose + N-acylsphingosine.
SUBCELLULAR LOCATION: Lysosomal (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GALACTOSYLCERAMIDE, GALACTOSYLSPHINGOSINE, LACTOSYLCERAMIDE, AND MONOGALACTOSYLDICLYCERIDE. ENZYME WITH VERY LOW ACTIVITY RESPONSIBLE FOR THE LYSOSOMAL CATABOLISM OF GALACTOSYLCERAMIDE, MAJOR LIPID IN MYELIN, KIDNEY AND EPITHELIAL CELLS OF SMALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: HYDROLYSES
sapiens (Human)
                                                                                                                                                                           IFFWI 583
                                                                                                                                                                                                    IFFWI
                                                                                                                                                                                                                                                                                                                                                                                                          o; IPR001286; GH_59.
F02057; Glyco_hydro_59,
PR00850; GLHYDRLASE59
                                                                                                                                                                                                    5
                                                                                                                                                                                                                                                                                                                                                                                             Glycosidase;
                                                                                                                                                                                                                                                                              669
                                                                                                                                                                                                                                                                                                                  363
387
543
586
                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                              AA;
                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                      26
669
363
387
543
586
158
639
75316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=8661004
                                                                                                                                                                                                                                       100.0%;
                                                                                                                                                                                                                                                     86.1%;
                                    (Galactosylceramide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GALACTOSYLSPHINGOSINE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VARIANTS
                                                                                                                                                                                                                                                                                                                                                                                             Glycoprotein;
                                                                                                                                                                                                                                                                              MW.
                                                                                                                                                                                                                                                                                                                                                                                                                     _59; 1.
                                                                                                                                                                                                                           Score 31; DB; Pred. No. 1.5
                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                          P ->
                                                                                                                                                                                                                                                                                                                 N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
                                                                                                                                                                                                                                                                                                                                                                    GALACTOCEREBROSIDASE
                                                                                                                                                                                                                                                                                                                                                                                protein; Signal; Disease
BY SIMILARITY.
                                                                                                                                                                                                                                                                              60E298B024EE154C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLD
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                                                                                                                                                                                                                                                                                         (IN GLD).
                                                                                                              669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SER-158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                        DB 1; Lo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ESTER BONDS OF NGOSINE, LACTOSYLCERAMIDE,
                                                                                                             ΑA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           as its content
                                    beta-galactosidase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Highland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Usage
                                                  (GALCERASE)
                                                                                                                                                                                                                                                   Length 669;
                                                                                                                                                                                                                                                                              CRC64;
                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Euteleostomi;
Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                уд
                                                                                                                                                                                                                                                                                                                               (POTENTIAL)
                                                                                                                                                                                                                                                                                                                   (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                             mutation
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VARIANTS GALLOTTONIAND COLON. HAS AN OPTIMAL PH BETWEEN 4.0 AND 4.4.

**MEDLINES** COLON.**

**Rafi M.A., Luz1 P., Zlotogora J., Wenger D.A.;

**Two different mutations are responsible for Krabbe disease in the Druze and Moslem Arab populations in Israel.**;

**Hum. Genet. 97:304-308(1996).

**In. Genet. 97:304-308(1996).

**I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VARIANTS GLD ASN-528 AND SER-583. MEDLINE-96198195; PubMed-8786069;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wenger D.A., Rafi M.A., Luzi P.;
"Molecular genetics of Krabbe disease (globoid cell leukodystrophy):
diagnostic and clinical implications.";
Hum. Mutat. 10:268-279(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 characterization.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Okada S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=97478285;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-94002192; PubMed-8399327;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VARIANTS GLD ALA-302 AND GLY-550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Urine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 27-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-98094242; Pu
Sakai N., Fukushima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM
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"Cloning and expression of cDNA encoding human galactocerebrosidase,
the enzyme deficient in globoid cell leukodystrophy.";
Hum. Mol. Genet. 2:1841-1845(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Brain, and Testis;
MEDLINE-94108435; PubMed-8281145;
Chen Y.Q., Rafi M.A., de Gala G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND PARTIAL SEQUENCE TISSUE-Placenta, and Skin fibroblast; MEDLINE-94128088; PubMed-8297359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tatsumi N., Inui K., Sakai N., Fukushima H.,
Yanagihara I., Nishigaki T., Tsukamoto H., F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=96121583;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biochim. Biophys.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Galactocerebrosidase from human urine: purification and partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human galactocerebrosidase gene: promoter region and structural organization."; siochim. Biophys. Acta 1395:62-67(1998).
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Tatsumi N., Ozono K., Okada S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           enomics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.,
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Yanagihara I., Isegawa Y., Iwamatsu A., Okada S.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genet.
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ma H., Inui K., Fu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed-8595408;
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GALACTOSE + N-ACYLSPHINGOSINE.

-!- SUBCELLULAR LOCATION: LYSOSOMAI.
-!- ALTERNATIVE PRODUCES: TWO FORMS ARE PRODUCED BY ALTERNATIVE
SPLICING. THE SEQUENCE SHOWN HERE IS THAT OF THE LONG FORM.

SPLICING. THE SEQUENCE SHOWN HERE IS THAT OF THE LONG FORM.

-!- TISSUE SPECIFICITY: HIGHEST LEVEL OF ACTIVITY IN TESTES COMPARED
TO BRAIN, KIDNEY, PLACENTA AND LIVER. CAN ALSO BE FOUND IN URINE.
-!- DISCASE: DEFECTS IN GALC ARE THE CAUSE OF GLOBOID CELL
LEUKODYSTROPHY (GLD) (OR KRABBE DISEASE). THIS AUTOSOMAL RECESSIVE
DISOMBED BETCIENCY RESULTS IN THE INSUFFICIENT CATABOLISM OF
SEVERAL GALACTOLIPIDS THAT ARE IMPORTANT IN THE PRODUCTION OF
NORMAL MYELIN. CLINICALLY THE MOST FREQUENT FORM IS THE INFANTILE
FORM, MOST PATIENTS (90%) PRESENT BEFORE SIX MONTHS OF AGE MITH
IRRITABILITY, SPASTICITY, ARREST OF MOTOR AND MENTAL DEVELOPMENT,
AND BOUTS OF TEMPERATURE ELEVATION WITHOUT INFECTION. THIS SPOLLOWED BY WYOCLONIC JERKS OF ARMS AND LEGS, OPOSTHOTONUS,
HYPERTONIC FITS, AND MENTAL REGRESSION, WHICH PROGRESSES TO A
SEVERE DECERBRATE CONDITION WITH NO VOLUNTARY MOVEMENTS AND DEATH
FROM RESPIRATORY INFECTIONS OR CEREBRAL HYDERYBRAIN BEFORE 2
YEARS OF AGE. HOWEVER, A SIGNIFICANT NUMBER OF CASES WITH LATER
ONSET, PRESENTING WITH UNEXPLAINED BLINDNESS, WEAKNESS AND/OR
PROGRESSIVE MOTOR, AND SENSORY NEUROPATHY THAT CAN PROGRESS TO
SEVERE MENTAL INCAPACITY AND DEATH, HAVE BEEN IDENTIFIED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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; PF02057; G1
rs; PR00850;
                                                L38557
L38557
L38588
D86181
D86123
D84233
D84234
D84267
D842667
D842669
D84363
D84363
D84363
D84365
                         245200;
                                                                                                                                                                                                                                                                                   L38544;
L38545;
                                                                                                                                                                                                                                                                                                                    D25283;
D25284;
                                                                                                                                                                                                  L38551
L38552
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L38556
                                                                                                                                                                                                                                          L38549;
L38550;
                 IPR001286;
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                                                                          BAA24902
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        Glyco_hydro_59;
GLHYDRLASE59
                 GH_59
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Query Match
Best Local Similarity
-----hes 5; Conserv
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                                                                                                                                        RESULT 11
                                                                                                                                                               В
                                                                                          GALC_MACMU
002791;
15-JUL-1999
15-JUL-1999
15-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hydrolase;
Disease mut
SIGNAL
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                         VARSPLIC VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
CARBOHYD
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CARBOHYD
                                                                  15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
Galactocerebrosidase precursor (EC 3.2.1.46) (GALCERASE)
(Galactosylceramidase) (Galactosylceramide beta-galactosidase)
(Galactocerebroside beta-galactosidase).
SEQUENCE FROM N.A. MEDLINE=97336058; PubMed=9192853;
                                       Eukaryota;
Mammalia; F
                                                                                                                                 MACMU
                                                                                                                                                                                                                                          VARIANT
                                                                                                                                                                                                                                                         VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                           VARIANT
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                                Cercopithecinae; Macaca.
                                                      Macaca mulatta (Rhesus macaque)
                                                                                                                                                                                                                                                                                      VARIANT
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                        NCBI_TaxID=9544;
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                                                                                                                                                               579
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                                                                                                                                                              |||||
|FFWI 583
                                       Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Glycosidase; Glycoprotein; Signal; Alternative splicing;
                                                                                                                                                                                            Conservative
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95
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                                                                                                                         STANDARD;
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                                                                                                                                                                                                   86.1%;
                                                                                                                                                                                           0;
                                                                                                                                                                                                   Score 31;
Pred. No.
                                                                                                                                                                                                                                 R -> W
SPOTS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GALACTOCEREBROSIDASE.
N-LINKED (GLCNAC...
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/FTId=VAR_003380.
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/FTId=VAR_003392.
                                                                                                                                                                                                                                                                                     /FTId=VAR_003390
N -> T (IN GLD).
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                                                                                                                                                                                                                                                                                                                                        I -> T (IN GLD; I
/FTId=VAR_003387.
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G -> A (IN GLD).
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                                       Craniata; V
Catarrhini;
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VAR_003389.
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1.5e+02;
                                       Vertebrata; Euteleostomi;
i; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                      , ADULT).
                                                                                                                                                                                                                                        BILATERAL CHERRY
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                                                                                                                                                                                                                                                                                                                                                                                                           ADULT).
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                                                                                                                                                                                                         Length 569;
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(POTENTIAL).
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                                                                                                                                                                                           0;
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                                                                                                                                                                                           0;
RESULT 12
ATY3_HUMAN
ID ATY3_HUMAN
AC Q9H7F0;
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                                                            QУ
                                                                            Matches
                                                                                  Query Match
Best Local
                                                                                                         CARBOHYD
CARBOHYD
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SEQUENCE
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CARBOHYD
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SIGNAL
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                                                             1 IFFWI 5
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U87463 AAB58575.1
U87464 AAB58575.1
U87466 AAB58575.1
U87466 AAB58575.1
U87466 AAB58575.1
U87467 AAB58575.1
U87468 AAB58575.1
U87470 AAB58575.1
U87470 AAB58575.1
U87471 AAB58575.1
U87472 AAB58575.1
U87473 AAB58575.1
U87473 AAB58575.1
U87473 AAB58575.1
U87473 AAB58575.1
                                              IFFWI
                                                                                                                                                                                                   PF02057;
                                                                          Similarity
5; Conserv
                                                                                                                                                                                          F02057; Glyco_hydro_59; PR00850; GLHYDRLASE59.
                                                                                                                                                                                                          IPR001286;
                                              583
                                                                                                        1
1
27
127
363
387
435
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543
543
                                                                                                                                                                                   Glycosidase;
                                                                            Conservative
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                                                                                                                                                                                                                  AAB58576
                                                                                                                                                                                                                        AAB58575.1;
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        STANDARD;
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668
1127
363
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387
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100.0%;
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                                                                                                                                                                                   Glycoprotein;
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JOINED.
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                                                                                                       GALACTOCEREBROSIDASE.
N-LINKED (GLCNAC...)
                                                                          Score 31; DB; Pred. No. 1.5
                                                                           0,
        PRT;
                                                                                                                                                                            SIMILARITY.
        684
                                                                                   DB 1;
1.5e+
        A
                                                                                  .5e+02;
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Length 669; CRC64;

(POTENTIAL).
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(POTENTIAL).
(POTENTIAL).

(POTENTIAL) (POTENTIAL)

Indels

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Gaps

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use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a c
between the Swiss Institute of Bioinformatics and the EMBL
the European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Luzi P., Rafi M.A., Victoria T., Baskin G.B., Wenger D.A.; "Characterization of the rhesus monkey galactocerebrosidase "Characterization identification of the mutation causing glo leukodystrophy (Krabbe disease) in this primate."; Genomics 42:319-324(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                            INTESTINE AND COLON (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: D-galactosyl-N-acylsphingosine
                                                                                                                                                                                                                                galactose + N-acylsphingosine.
SUBCELLULAR LOCATION: Lysosomal (By similarity).
DISEASE: DEFECTS IN GALC ARE THE CAUSE OF GLOBOID CELL
LEUKODYSTROPHY (GLD) (OR KRABBE DISEASE). THIS DEFICIENC
IN THE INSUFFICIENT CATABOLISM OF SEVERAL GALACTOLIPIDS
IMPORTANT IN THE PRODUCTION OF NORMAL MYELIN.
SIMILARITY: BELONGS TO FAMILY 59 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: HYDROLYSES THE GALACTOSE ESTER BONDS OF GALACTOSYLCERAMIDE, GALACTOSYLCERAMIDE, ANI MONOGALACTOSYLCERAMIDE, GALACTOSYLCERAMIDE, ANI MONOGALACTOSYLCERAMIDE, ENZYME WITH VERY LOW ACTIVITY RESPONSIBLE FOR THE LYSOSOMAL CATABOLLSM OF GALACTOSYLCERAMIDE, MAJOR LIPID IN MYBLIN, KIDNEY AND EPITHELIAL CELLS OF SMALL
                              (See http://www.isb-sib.ch/announce/
                                                                                        as its content
                                                            Usage
                                                                                                                                                                                                                                                                                                                               OID CELL
DEFICIENCY
                                                            Ьy
                                                                                                                      restrictions
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coutstation -
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                                                               commercia.
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between
                                                                             Bacteria; Proteobacteria;
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                                                                                                                                                                               01-FEB-1995
16-OCT-2001
                                                                                                                                                                                                                                            TRD1_ECOLI P09130;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KAWABDATA A., HÎK1]Î T., KODATAKE N., INAGAKÎ H., IKEMA Y OXÎTANÎ R., OTA T., SUZUKÎ Y., ODAYASÎÎ M., NÎSÎÎ T., SÎ
TANAKA T., NAKAMUTA Y., ISOYAÎ T., SUÇAN S.;
"NEDO human cDNA sequencing project.";
SUBMÎLTE (AUG-2000) to the EMBL/GenBANK/DDBJ databases.
-!- CATALYTIC ACTIVITY: ATP + H(2)0 = ADP + phosphate.
-!- SUBCELLUJAR LOCATION: Integral membrane protein (By
SEQUENCE
                                                          Escherichia
                                                                                                  Plasmid F.
                                                                                                                     Escherichia
                                                                                                                                                                                                                     01-MAR-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long a modified and this statement is not removed.
                                     NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AK024639; BAB14942.1; ALT_INIT.
InterPro; IPR001757; ATPase_E1-E2.
InterPro; IPR001454; H1gnase/hydrlase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Probable cation transporting ATPase 3 (EC 3.6.3.-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. TISSUE-Coronary ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSMEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PF00702; Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              486
684 AA;
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(Rel.
(Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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44
537
568
602
659
                                                                                                                                                                                                                                                               STANDARD;
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31,
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Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86.1%;
80.0%;
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Last
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                                                                                                                                                                             sequence up
annotation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 31;
Pred. No.
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Lee M.H., Kosuk N., Bailey J., Traxler B., Mane "Analysis of F factor TraD membrane topology by and trypsin sensitive insertions.";
J. Bacteriol. 181:6108-6113(1999)
-i- FUNCTION: TRAD IS A CELL ENVELOPE PROTEIN.
IS UNKNOWN BUT IT IS ESSENTIAL FOR DNA TRAN MAY BE PART OF A NON-SPECIFIC PORE FOR DNA
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MEDLINE-94359430; PubMed-7915817;
MEDLINE-94359430; PubMed-7915817;
Frost L.S., Ippen-Ihler K., Skurray
"Analysis of the sequence and gene"
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                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=90317835; PubMed=2164585; Yoshioka Y., Fujita Y., Ohtsubo E.; "Nucleotide sequence of the promoter-distal region of the of plasmid R100, including tral (DNA helicase I) and trab J. Mol. Biol. 214:39-53(1990).
                                    between the Swiss Institute of Bioinformat
the European Bioinformatics Institute. The
use by non-profit institutions as long
modified and this statement is not removed.
                                                                              This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Surface exclusion genes tras and traff of the F sex factor of Escherichia coli K-12. Determination of the nucleotide sequent promoter and terminator activities.";

J. Mol. Biol. 198:1-11(1987).
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                                                                                                                                                                                                                                                                     MEDLINE=99429860; PubMed=10498725;
                                                                                                                                                                                                                                                                                  TOPOLOGY
                                                                                                                                                                                                                                                                                                             "Purification and properties of the F sex factor TraD protein, inner membrane conjugal transfer protein.";
J. Biol. Chem. 267:12761-12766(1992).
                                                                                                                                                                                                                                                                                                                                                        Panicker M.M., Minkley E.G. Jr.;
                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=92316963;
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Shimizu H., Saitoh
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MEDLINE-90317835; PubMed-2164585;
YOShioka Y., Fujita Y., Ohtsubo E.;
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                actin-severing domains.";
Protein Sci. 6:1197-1209(1997)
                                                                                                                                                                                                                          STRUCTURE BY NMR OF 1-127 MEDLINE=94191534; PubMed=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=88276884; PubMed=2839826; Bazari W.L., Matsudaira P., Wallek M.,
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                                                      Markus M.A., Matsudaira P., Wagner G 
"Refined structure of villin 14T and
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                                                                                                                                                       Protein
                                                                                                                                                                                                              Markus M.A., Nakayama T.,
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"Demonstration of three distinct calcium-binding
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sci. 3:70-81(1994).
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m. 258:365-369(1983).
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10 X 3 AA TANDEM REPEATS
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PIR; A03082; A03082.
PIR; A31822; A31822.
PDB; 2VIK; 01-APR-97.
PDB; 1VII; 11-AUG-97.
InterPro; IPR001974 Gelsolin.
InterPro; IPR001974 Gelsolin.
Pfam; PF00626; Gelsolin; 6.
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SMART; SM00262; GEL; 6.
SMART; SM00153; VHP; 1.
Cytoskeleton; Calcium; Actin-binding; Capping protein; Repeat;
3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MCKNIGHT C.J., MATSUGAIRA P.T., KIM P.S.;

"NMR STRUCTURE OF the 35-residue villin headpiece subdomain.";

NAT. STRUCT. Biol. 4:180-184(1997).

-I- FUNCTION: CA(2+)-REGULATED ACTIN-BINDING PROTEIN. ITS CAPPING FUNCTION IS LOCALIZED TO DOMAIN I; ITS SEVERING ACTION IS A COOPERATION BETWEEN AN F-ACTIN BINDING SITE OF DOMAIN II AND THE CAPPING ACTIVITY OF DOMAIN I.

-I- SUBJUNT: MONOMER.
-I- TISSUE SPECIFICITY: COMPONENT OF BRUSH BORDER MICROVILLI.
-I- SIMILARITY: BELONGS TO THE VILLIN/GELSOLIN FAMILY.
-I- SIMILARITY: CONTAINS 6 GELSOLIN-LIKE REPEATS.
                                                                   SEQUENCE
                                                                                                                                                                                                                                                                   SITE
                                                                                                                                                                                                                                                                                                                                                                       REPEAT
REPEAT
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GELSOLIN-LIKE 3.
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GELSOLIN-LIKE 5.
GELSOLIN-LIKE 5.
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9: sp_phage:*
10: sp_plant:*
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Q95x16 caenorhabdi
Q93x66 chlorobium
Q9z6d5 haemophilus
Q91fw6 chilo iride
Q9a628 caulobacter
Q9a628 vibrio para
Q36329 chondrus cr
Q8vn11 lactobacil1
Q9pw03 labeo rohit
Q9cmx2 pasteurella
Q91698 lactobacil1
Q8vn06 lactobacil1
Q8vn06 lactobacil1
Q8vn06 fagus sylva
Q8ujd6 agrobacteri
Q91ej5 human calic
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Bauer B.A., Lumbley S.R., Hansen E.J.;
"Characterization of a Waaf (Rfaf) hom
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Molecular evidence for the early evolution
Science 289:1724-1730(2000).
EMBL: AY005138; AAG12430.1;
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Identification of genes encoding zinc finger chromosomal HMG protein homologue, and a putat in the genome of Chilo iridescent virus.";

Nucleic Acids Res. 22:158-166(1994).
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Q91FW6;
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MEDLINE-92196996; PubMed-1549908;
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"DNA analysis of insect iridescent vir
permutation and terminal redundancy.";
J. Virol. 49:609-614(1984).
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SEQUENCE FROM N.A.
Darai G.,
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MEDLINE=93260401; PubMed=8492091;
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Fischer M., Schnitzler P., Delius H., Darai G.;
Fischer M., Schnitzler P., Delius H., Darai G.;
"Identification and characterization of the repetitive
the genome of insect iridescent virus type 6.";
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MEDLINE-87321126; PubMed-2820141;
Schnitzler P. Soltau J.B., Fisch
Delius H., Darai G.;
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Viruses; dsDNA viruses, no RNA stage; Iridoviridae; Iridovirus
    MEDLINE=94353641;
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Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF303741; AAK82066.1; -.
SEQUENCE 62 AA; 7876 MW; 29DF67A85F664B3E CRC64;
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"Analysis of the First Complete DNA Sequence Iridovirus: Coding Strategy of the Genome of Virology 286:182-196(2001).
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Virus Genes 18:243-264(1999).
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J. Gen. Virol. 75:1557-1567(1994).
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MEDIANE-21/13698; PubMed=11259647;
Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K. Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R., Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., El DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H., Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., Whi Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.; "Complete genome sequence of Caulobacter crescentus."; Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
                                                                                                                TIGRFAMs; Flagella.
                                                                                                                                                                                                                                                                              "Components of the po
apparatus.";
Submitted (MAR-2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                "Insertional inactivation of genes encoding components of the sodium-type flagellar motor and switch of vibrio parahaemolyticus."; J. Bacteriol. 182:1035-1045(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vibrio parahaemolyticus
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STRAIN=ATCC 19089 / CB15;
MEDLINE=21173698; PubMed=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=BB22
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Pro; IPR002920; YscJ_FliF.
PF01514; YscJ_FliF; 1.
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Q1-MAR-2002 (TrEMBLrel. 20, Las
Lactobacillus delbrueckii (subs
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Q36329;
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J. Mol. Evol. 41:196-202(1995).
EMBL; 247547; CAA87598.1;
                                                      Bourniquel A.A., Casey M.G., Mollet B., "DNA sequence and functional analysis of subsp. lactis plasmids pN42 and pJBL2." plasmid 0:0-0(0).
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"Complete sequence of the mitochondrial DNA of the rhodophyte Chondrus crispus (Gigartinales). Gene content and genome organization.";

J. Mol. Biol. 250:484-495(1995).
  EMBL; AJ421486;
Plasmid
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SEQUENCE 73
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Leblanc C., Boyen
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NCBI_TaxID=29397;
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71 LFFWVK 76
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                                    CAD13351.1;
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C., Richard O.,
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NCBI_TaxID=84645;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Rohu liver hypothetical protein (Fragment).
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                                        Hypothetical protein; Complete SEQUENCE 120 AA; 14167 MW;
                                                            May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam "Complete genomic sequence of Pasteurella multocida Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
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                                                                                                                                                                                                  Hypothetical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                     MEDLINE=21145866; PubMed=11248100;
                                                                                                                                              NCBI_TaxID=747;
                                                                                                                                                         Pasteurella
                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein.
                                                                                                                        EQUENCE FROM N.A.
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           Local
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nes 4; Conserv
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Similarity
5; Conser
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ilarity 100.0%;
Conservative
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66.7%;
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                    88.9%;
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Pred. No.
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          Score 32;
Pred. No
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                                        proteome.
46308C480002FF64 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                       6E36D649DA8FFB08 CRC64;
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                                                                                                                                                                   subdivision; Pasteurellaceae;
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 Mismatches
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                      DB 16;
                                                                                                                                                                                                                                                                                                                                                                  DB 13;
           1.3e+02;
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Matches 4
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Best Local S
Matches 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9L6G8 PRELIMINARY; PRT; 174 AA.
Q9L6G8;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
 Q98QA5
                                                                                                                                                                                                                                                                               Plasmid 0:0-0(0).
EMBL; AJ421627; CAD15746.1;
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AZCARZÍE M.A., RAYA R.R.;
AZCARZÍE M.A., RAYA R.R.;
AZCARZÍE M.A., RAYA R.R.;
AZCARZÍE M.A., RAYA R.R.;
Submitted (FEB-2000) to the EMBL/
Submitted (FEB-2000) to the EMBL/
                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

Bourniquel A.A., Casey M.G., Mollet B.,
"DNA sequence and functional analysis of
subsp. lactis plasmids pN42 and pJBL2."
                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Firmicutes; Bacillus/Clostridium Lactobacillaceae; Lactobacillus. NCBI_TaxID=29397;
                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                Hypothetical protein; Plasmid.
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Lactobacillaceae; Lactobacillus.
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                                                                                                                                                                                       Similarity
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 PRELIMINARY;
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66.7%;
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                                                                                                                                                                  Score 32; DB Pred. No. 1.8e 2; Mismatches
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Pred. No. 1.8e+02;
 PRT;
                                                                                                                                                                                                                                            278D0FB317C001D9 CRC64;
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                                                                                                                                                                                                                                                                                                                   B., Pridmore R.D.;
s of Lactobacillus c
2.";
 423
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 B
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                                                                                                                                                                                                       Length 1.74;
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                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                          delbrueckii
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DDDRRRACE RRECTED DO CONTRACTOR OF THE CONTRACTO
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Query Match
Best Local S
Matches 4
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01-MAR-2001 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                          Universidad de Salamanca.
-!- SIMILARITY: BELONGS TO THE SER/THR EMBL; AJ298993; CAC09581.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                             Fagus sylvatica (Beechnut).
Eukaryota; Viridiplantae; Stra
Spermatophyta; Magnoliophyta;
eurosids I; Fagales; Fagaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-UN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical protein MYPU_4610.
                                                                                                                                                                                                                                         (In) Black M., Bradford K.J., Vazquez-Ramos SEED BIOLOGY-ADVANCES AND APPLICATIONS 32, p
                                                                                                                                                                                                                                                                             like gene, which are regulated sylvatica seeds.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9FDV6
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Hypothetical protein; Complete proteome.
SEQUENCE 423 AA; 50819 MW; B4A027C3E9264F9E
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Nucleic Acids Res. 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=21267165; PubMed=11353084;
Chambaud I., Heilig R., Ferris S., Barbe V., S.
Moszer I., Dybvig K., Wroblewski H., Viari A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mycoplasmataceae;
NCBI_TaxID=2107;
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       InterPro;
                      InterPro;
                                       InterPro;
                                                                                                                                  Thesis (2000),
                                                                                                                                                                       TISSUE-SEED;
                                                                                                                                                                                                                            CAB international,
                                                                                                                                                                                                                                                                                            Lorenzo O., Rodriguez D., Nicolas C., N. "Characterization and expression of two like gene, which are regulated by ABA a
                                                                                                                                                                                                                                                                                                                                                     TISSUE=SEED;
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=28930;
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                                                          InterPro;
                                                                                                                                                    Corenzo 0
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IPR004477; ComEC_N-term.
IPR001064; Crystallin.
IPR000719; Euk_pkinase.
IPR002290; Ser_thr_pkinase.
IPR001245; Tyr_pkinase.
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                                                                                                                                 Fisiologia
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16,
21,
                                                                                                                               Vegetal, Facultad de Biologia,
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/ta; eudicotyledons;
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Last annotation update)
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Pred. No.
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wo protein kinase genes
and GA3 in dormant Fagu
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pp.329-340,
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eudicots; Rosid
                                                                                                KINASES
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Best Local
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Ourcollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
Houmiel K., Gordon J., Yaudin M., Iartchouk O., Epp A., Liu F.,
Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
Clelo C., Slater S.,
"Genome sequence of the plant pathogen and biotechnology agent
Agrobacterium tumefaciens C58.";
Science 294:2323-2328(2001).
EMBL; AE008974; AAL46227.1; ALT_INIT.
EMBL; AE007922; AAK90918.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OBUJD6 PRELIMINARY: PRT; 671 AA.
OBUJD6;
O1-JUN-2002 (TrEMBLrel. 21, Created)
O1-JUN-2002 (TrEMBLrel. 21, Last sequence update)
O1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical protein Atu5541.
ATU5541 OR AGR_PAT_807.
AGROBACTERIUM tumefaciens (strain C58 / ATCC 33970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P., Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L., Chen Y., Paulsen I.T., Elsen J.A., Karp P.D., Bovee D. Sr., Chapman P., Clendenning J., Deatherage G., Gillett W., Grant C., Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A., Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A., Kutyavin T., Cevy R., Li M.-J., McClelland E., Palmieri A., Romero P., Gordon D., Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D., Raymond S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M., Gordon Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M., Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V., Nester E.W.;
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SMART; SM00220; S_TKC; 1.
SMART; SM00219; TYTKC; 1.
PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
ATP-binding; Kinase; Serine/Chreonine-protein kinase; Transferase.
SEQUENCE 666 AA; 74385 MW; DA586B1276259C97 CRC64;
                                                                                                                                                  Hypothetical protein; Plasmid; Complete proteome. SEQUENCE 671 AA; 72766 MW; 43EDB89528813482 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-21608551;
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Science 294:2317-2323(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The genome of the natural genetic engineer Agrobacterium tumefaciens {\sf C58."};
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE=21608550; PubMed=11743193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Rhizobium.
NCBI_TaxID=176299;
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369 IFFWIE 374
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5; Conserv
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5; Conserv
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                                                                            Conservative
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                                                                                            88.98;
                                                                      Score 32; DB 16; Length 671; Pred. No. 6.1e+02; l; Mismatches 0; Indels
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6e+02;
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Search completed: January 3, 2003, 15:32:03 Job time: 21.3182 secs

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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/1,
2: /cgn2_6/ptodata/1,
3: /cgn2_6/ptodata/1,
4: /cgn2_6/ptodata/1,
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6: /cgn2_6/ptodata/1,
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Match
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Gapop 10.0 ,
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   262574 seqs, 29422922 residues
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
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/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
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2 US-08-477-451-7

2 US-08-336-031-4

5 PCT - US-55-06725-4

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5 PCT - US-95-06725-2

1 US-08-968-982-2

1 US-08-96-988-2

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4 US-08-678-194-8

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19.615 Million cell updates/sec
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Qy Db	Qu Be Ma	US :		
1 679	ery st I tche	SULT 1 Sequence 7, Applicat Patent No. 5928865 GENERAL INFORMATION APPLICANT: COVVAC: TITLE OF INVENTIO NUMBER OF SEQUENC CORRESPONDENCE AD ADDRESSEE: Chi STREET: 4560 H CITY: Emeryvil STATE: CA ZIP: 94608-291 COMPUTER READABLE MEDIUM TYPE: F COMPUTER: IBM OPERATING SYSTE SOFTWARE: Pate CURRENT APPLICATION NUM PILING DATE: O CLASSIFICATION NUM REFERENCEDOCKE TELEPHONE: 510-6 INFORMATION FOR SEQ SEQUENCE CHARACTE LENGTH: 3287 an TYPE: amino ac STRANDEDNESS: TOPOLOGY: 1ine MOLECULE TYPE: p 1-08-4477-451-7		4 4 4 4 4 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0
IFFWIK :	h Simi 5;	HT 1 8-477-451-7 quence 7, Application U quence 7, Application U tent No. 5928865 ENERAL INFORMATION: APPLICANT: COVACCÍ, A TITLE OF INVENTION: APPLICANT: COVACCÍ, A TITLE OF INVENTION: APPLICATION: ADDRESSE: Chiron C STREET: 4560 HOTCON CITY: Emeryville STATE: CA COUNTRY: USA ZIP: 94608-2916 COMPUTER READABLE FORM MEDIUM TYRE: J1M PC COMPUTER: IBM PC OPERATING SYSTEM: P SOFTWARE: PATENTION NUMBER: FILING DATE: 07-JUN CLASSIFICATION UMBER: FILING DATE: 07-JUN CLASSIFICATION INFORMAN NAME: MCCLUNG, Barb REGISTRATION INFORMAN NAME: MCCLUNG, Barb REGISTRATION INFORMAN NAME: MCCLUNG, Barb REGISTRATION FOR SEQ ID N SEQUENCE CHARACTERISTI LENGTH: 3287 amino TYPE: amino acid STRANDEDNESS: singl TOPOLOGY: linear MOLECULE TYPE: protei		22222222222222222222222222222222222222
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	Score 34; DB 2; Length Pred. No. 5.5e+02; 1; Mismatches 0; Ind	US/08477451 Antonello Helicobacter Pylori Cagi Region S: Corporation n Street M: y disk ompatible PC-DOS/MS-DOS Release #1.0, Version #1.30 ATA: US/08/477,451 N-1995 ATION: bara G. bara G. 33.113 MHS 3.113 MHS 3.133 MHS 3.133 MHS 3.133 MHS 3.113 MHS 3.11	ALIGNMENTS	US-08-747-221B-14 US-09-005-051-14 US-08-747-221B-53 US-09-005-051-53 US-09-005-051-19 US-08-747-221B-58 US-09-005-051-58 US-09-005-051-58 US-09-165-396-3 US-08-340-011-2 US-08-340-011-2 US-08-88-74-678-33 US-08-8874-678-33 US-08-8874-678-33 US-08-643-839-33
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	3287; els			Sequence
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	Gaps			14, Appl 53, Appl 53, Appl 19, Appl 19, Appl 19, Appl 19, Appl 10, Appl 11, Appl 11, Appl 12, Appl 13, Appl 13, Appl 13, Appl 13, Appl 13, Appl 13, Appl 13, Appl 13, Appl 14, Appl 15, Appl 16, Appl 17, Appl 18, Appl 18, Appl 19,
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RESULT

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Matches
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Patent No. 5817782
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TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/253
FILING DATE: 03-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: DIG19110, Frank S.
REGISTRATION NUMBER: 31,346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acids
TYPE: amino acid
TOPOLOGY: line
CURRENT APPLICATION DATA:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,031
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                    CITY: Garden City
STATE: New York
                                                                                                                                                                      ADDRESSEE: Scully, Scott, Murphy & Presser STREET: 400 Garden City Plaza
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OPERATING SYSTEM: PC-DOS/MS-DOS
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STATE: New York
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(516) 742-4366
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VENTION: LAG1:
                                                                                                                     United States
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                              FILING DATE: 514
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
OFFICE DATE: 03-JUN-1994
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INFORMATION FOR SEQ ID NO:
                                                                                        TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 2
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
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LENGTH: 218 amino acid
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
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PRIOR APPLICATION DATA:
                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 411 amino acid
                                                                                                                                            REFERENCE/DOCKET NUMBER: 93
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
                                                                                                                                                                                                                     FILING DATE: 03-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: DiGiglio, Frank S.
                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,031
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Jazwinski, S. M.
TITLE OF INVENTION: LAG1: A GENE
TITLE OF INVENTION: LONGEVITY OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION: NAME: DiGiglio, Frank S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         118 VFFWI 122
                                                                                                                                                                                                 REGISTRATION NUMBER: 31,346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 11530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Garden City
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 08/253,875 & 08/336,031 FILING DATE: 03-JUN-1994 & 08-NOV-1994
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                     TOPOLOGY:
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                            H: 411 amino acids
amino acid
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US-08-902-853-7
; Sequence 7, Application US/08902853
; Patent No. 5945330
RESULT 6
PCT-US95-06725-2
; Sequence 2, Application PC/TUS9506725
; GENERAL INFORMATION:
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Best Local Similarity 80.0
1-2hes 4; Conservative
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APPLICANT:
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APPLICANT: Lal, Preeti
TITLE OF INVENTION: HUMAN LONGEVITY-ASSURANCE PROTEIN HOMOLOGS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/902,853
FILING DATE: Herewith
                                                                                                                                                                                                                                    IMMEDIATE SOURCE:
LIBRARY: GenBa
CLONE: 541568
                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 411 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Billings, Lucy J. 749
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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MEDIUM TYPE: Diskett
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ATTORNEY/AGENT INFORMATION:
                                                                                              311 VEFWI 315
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nes 4; Conserv
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CITY: Palo Alto
STATE: CA
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STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 415-845-4166
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Corley, Neil C.
Shah, Purvi
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Pred. No. 3.7e+02;
                                                                                                                                                        Mismatches
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US-08-844-064-7
; Sequence 7, Application US/08844064
; Patent No. 5747314
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Best Local Similarity
Thehes 4; Conserva
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 2:
SOFTWARE: FASTSEM: DOS

SOFTWARE: FASTSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/844,064
FILING DATE: 18-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION: 435
                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
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LENGTH: 411 amino acid
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NAME: DiGiglio, Frank S.
REGISTRATION NUMBER: 31,
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APPLICATION NUMBER: US 08/253,875 & 08/336,031
FILING DATE: 03-UN-1994 & 08-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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ADDRESSEE: SmithKline
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                     APPLICANT: Lawlor, TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   311 VFFWI 315
                                                                                                                                                                                                               STREET: 709 Swedeland CITY: King of Prussia STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: PCT/US95/06725 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 400 Garder CITY: Garden City
                                                                                                                                                                              COUNTRY: USA
ZIP: 19406-0939
                                                                                                                                                                                                                                     ADDRESSEE: Smiling.
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Pred. No. 3.7e+02;
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TYPE: amino acid
STRANDEDNESS: sinc
TOPOLOGY: linear
MOLECULE TYPE: prote
US-09-009-433-7
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Patent No. 6087142
GENERAL INFORMATION:
                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 08/844,064
APPLICATION NUMBER: 08/844,064
FILING DATE: 18-APR-1997
APPLICATION NUMBER: 9607991.8
FILING DATE: 18-APR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 uery Match
                                                                                                         INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 423 amino acids
                                                                                                                                                                           NAME: Gimmi Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P31458-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/009,433
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ADDRESSEE: SmithKline Beecham Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: No. 6087142el Compounds NUMBER OF SEQUENCES: 10
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ZIP: 19406-0939
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                                                                                         LENGTH:
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                                                                                           423
                                                                                                                                                            610-270-5090
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linear
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Query Match
Best Local Similarity
Thomas 4; Conserve
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US-08-068-392-2
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                                                                                                                                                                                         us-08-396-988-2
                                                                                                                                                                                                         RESULT 10
                                                                                                                                                          Sequence 2, Application US/08396988 Patent No. 6204043
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Best Local Similarity
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                                                                                                                              GENERAL INFORMATION:
APPLICANT: Shapire
                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (314)694-5435
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 470 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                 APPLICANT: Shapiro, TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Meyer, Scott J.
REGISTRATION NUMBER: 25275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING.SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 07
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)694-3117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Shapiro, TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                  305 FFWLK 309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: 199305 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING.SYSTEM: PC-DOS/MS-DOS
COUNTRY: USA
ZIP: 63167
                           STATE:
                                         STREET: 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                               2 FFWIK 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
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: Missouri
                                                                                                                                                                                                                                                                                                                                                                                                               AMINO ACID
                           Missouri
                                                                                                                                                                                                                                                                                                                                                                                                                           470 amino acids
                                                      800 N. Lindbergh Blvd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Scott J. Meyer, Monsanto Co., A3SM 800 N. Lindbergh Blvd.
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                                                                                                                                                                                                                                                                                                            Conservative
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                                          Louis
                                                                    Scott J
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                                                                                                                Human Macrophage Metalloproteinase
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                                                                                                                               Steven M.
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                                                                     Meyer, Monsanto Co., A3SM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US/08/068,392
                                                                                                                                                                                                                                                                                                        Score 30; DB 4; DC Pred. No. 4.2e+02;
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Pred. No. 3.8e+02,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Version #1.25
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RESULT 12
US-08-475-894-2
; Sequence 2, Application US/08475894
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US-09-391-104-26
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; MOLECULE TYPE:
US-08-396-988-2
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                                                                                                                                                                                                                  ; LENGTH: 470
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-391-104-26
                                                                                                                                                                                                                                                                                  SOFTWARE: 1
SEQ ID NO 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
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Best Local Similarity
                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Abbott Laboratories
APPLICANT: Falduto, Michael T.
APPLICANT: Magnuson, Scott R.
APPLICANT: Morgan, Douglas W.
TITLE OF INVENTION: HUMAN MATRIX METALLOPROTEASE GENE,
TITLE OF INVENTION: PROTEINS ENCODED THEREFROM AND METHODS
TITLE OF INVENTION: OF USING SAME
TITLE OF INVENTION: OF USING SAME
TILE REFERENCE: 6073.US.Pl
CURRENT FILING DATE: 1999-09-07
CURRENT FILING DATE: 1999-09-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/396
FILING DATE: 01-MAR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/068
FILING DATE: 28-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Meyer, Scott J.
REGISTRATION NUMBER: .07-2
REFERENCE/DOCKET NUMBER: .07-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314/694-3317
                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1997-
                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
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                                                                                   305 FFWLK 309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                  2 FFWIK 6
                                                                                                                                                   4;
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                                                                                                                                                                                                                                                                                                   FastSEQ for Windows Version 3.0
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                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (314)694-5435
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28-MAY-1993
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IBER: US 08/814,394
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                                                                                                                                                 Score 30; DB Pred. No. 4.2e.
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 30; DB 4;
Pred. No. 4.2e+02;
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                                                                                                                                               1.2e+02;
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US-08-484-710-2

: Sequence 2, Application US/08484710

; Patent No. 5656438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,894
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: LOUIS MYETS
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: BG:
                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acid
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TITLE OF INVENTION: THE CAIP-LIKE GENE FAMILY
                  ATTORNEY/AGENT INFORMATION:
NAME: Louis Myers
                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Yen-Ming Hsu
TITLE OF INVENTION: THE CAIP-LIKE GENE FAMILY
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                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
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CITY: Boston
                                                 FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                 STATE:
                                                                                                                                                                                                                                                              STREET: 60 St
CITY: Boston
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NAME: Louis Myers
REGISTRATION NUMBER:
                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
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                                                                                                                                                                                                                                                                                60 State Street,
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internal
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                                                                                                                      Release #1.0, Version
                                                                                       US/08/484,710
                                                                                                                                                                                                                                                                                Suite 510
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BGP-190

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TOPOLOGY: 1in
; MOLECULE TYPE:
; FRAGMENT TYPE:
; FRAGMENT TYPE:
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RESULT 15
US_08-474_697-2
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                                                                                                                                  Matches
                                                                                                                                               Query Match
Best Local Similarity
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Patent No. 5837844
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                        TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
                                                                                                                                                                                                                                                                                                     ATTORNEY AGENT INFORMATION:

NAME: LOUIS MYSTS
REGISTRATION UMBER: 35,965
REFERENCE/DOCKET NUMBER: BGP-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (617)227-594 INFORMATION FOR SEQ ID NO:
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MOLECULE TYPE:
FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,709
FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Yen-Ming Hsu
TITLE OF INVENTION: THE CAIP-LIKE GENE FAMILY
NUMBER OF SEQUENCES: 6
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ADDRESSEE: LAHIVE & COCKFIELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
TYPE: amino acid
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CITY: Boston
STATE: Massac
                                                                     68 IFFWV 72
                                                                                                                                                                                                                                                          TYPE: amino acids
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                                                                                                  1 IFFWI 5
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                                                                                                                                  4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 State Street, Suite 510
                                                                                                                                                                                                                                              linear
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internal
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internal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
                                                                                                                                             Score 30; DB 2;
Pred. No. 4.9e+02;
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Pred. No. 4.9e+02;
                                                                                                                                  Mismatches
                                                                                                                                                            Length 553;
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                                                                                                                              0;
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MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-474-697-2
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Search completed: January
Job time : 10 secs
                                                                                                                                 Query Match
Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                            TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/474,697
                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LOUIS Myers
REGISTRATION NUMBER: 35,1
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acid
                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Yen-Ming Hsu
TITLE OF INVENTION: THE CAIP-LIKE GENE FAMILY
                                                                     68 IFFWV 72
                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE:
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CITY: Boston
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80.0%;
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                                                                                                                                   Score 30; DB 4; Lo
Pred. No. 4.9e+02;
1; Mismatches 0;
                                                                                                                                                                   Length 553;
                                                                                                                                     0,
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Database :
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            al number of hits satisfying chosen parameters:
Published_Applications_AA:*

1: /cgn2_6/ptodata/1/pubpaa/U;

2: /cgn2_6/ptodata/1/pubpaa/U;

3: /cgn2_6/ptodata/1/pubpaa/U;

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length: 2000000000
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23.825 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 117078 seqs, 18951520 residues
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	35	97.2	487	و و	US-09-738-626-6481	Sequence 6481, Ap
2	31	86.1	53	10	US-09-864-761-40676	Sequence 40676, A
ω	31	86.1	58	10	US-09-867-550-866	Sequence 866, App
4	31	86.1	79	10	US-09-205-658-325	325,
ហ	31	86.1	951	10	US-09-815-242-10465	10465
6	31	86.1	951	10	US-09-815-242-13853	
7	31	86.1	1256	10	US-09-935-291A-6	
8	30	83.3	137	10	US-09-867-550-832	83
9	30	83.3	312	10	US-09-393-634-51	
10	30	83.3	445	9	US-09-992-598-177	177,
11	30	83.3	445	9	US-09-989-293A-177	
12	30	83.3	445	9	US-10-063-547-32	Sequence 32, Appl
13	30	83.3	445	9	US-09-989-735-177	
14	30	83.3	445	9	US-09-990-444-177	177,
15	30	83.3	445	9	US-09-989-730-177 •	
16	30	83.3	445	9	US-09-990-436-177	177,
17	30	83.3	445	9	US-09-991-181-177	Sequence 177, App
18	30	83.3	445	ဖ	US-09-993-687-177	Sequence 177, App
19	30	83.3	445	10	US-09-989-722-177	Sequence 177, App

45	44	43	42	41	40	.39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20
29	30	30	30	30	30	30	30	30	30	30	30	30	30	30	30	30	30	30	30	30	30	30	30	30	30
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34	954	950	883	883	880	879	877	876	810	473	470	470	445	445	445	445	445	445	445	445	445	445	445	445	445
10	10	10	10	10	10	10	10	10	10	10	10	9	12	12	10	10	10	10	10	10	10	10	10	10	10
US-09-864-761-49024	US-09-815-242-11238		US-09-815-242-13684	US-09-815-242-13382	US-09-815-242-10675 .	US-09-815-242-5312	US-09-815-242-4876	US-09-815-242-13003	US-09-815-242-12636	US-09-925-301-1217	US-09-801-196-23	US-09-920-455-219	US-10-052-586-148	US-10-006-867-32	-09-989-721-	US-09-990-456-177	US-09-993-604-177	US-09-991-163-177	-990-442-	US-09-991-073-177	US-09-989-732-177	US-09-989-731-177	US-09-989-727-177	US-09-989-279-177	-723-
Sequence 49024, A	11238,	Sequence 11961, A	Sequence 13684, A	13382,	-				12636	Sequence 1217, Ap	23,	219, 1	148	32,	177	177	Sequence 177, App	177		Sequence 177, App	177	177		177	

ALIGNMENTS

US-09-738-626-6481

Sequence 6481, Application US/09738626 Publication No. US20020197605A1

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                                                                                                                              ; TYPE: PRT; ORGANISM: Corynebacterium glutamicum US-09-738-626-6481
                                                                                                                                                                                                                                                                         APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
FULE RAPPLICATION UMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
                                                                                                                                                                          PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver. 3.0
SEQ ID NO 6481
LENGTH: 487
                                                               Query Match
Best Local Similarity
Matches 5; Conserv
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412 VFFWIK 417
                              1 IFFWIK 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MIZOGUCHI, HIROSHI
ANDO, SEIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                             TATEISHI, NAOKO
SENOH, AKIHIRO
                                                                                                                                                                                                                                                                                                                                                                                                                             IKEDA, MASATO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YOKOI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OCHIAI, KEIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HAYASHI,
                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HARUHIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MIKIRO
                                                                              97.2%;
83.3%;
                                                                              Score 35;
Pred. No.
                                                               Mismatches
                                                                                 . 33;
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                                                                                           Length 487;
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Matches
                         Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
                                                                                                                           OTHER INFORMATION: MAP TO ACO15473.3

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4.0

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.9

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.6

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.4

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.4

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.0

OTHER INFORMATION: EXPRESSED IN BARIN, SIGNAL = 4.1

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.1

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.1

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OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.1

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.1

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US PRIOR FILING DATE: 2000-08-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/207,456 PRIOR FILING DATE: 2000-05-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/180,312 PRIOR FILING DATE: 2000-02-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: Aeomica-X-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 ID NO 40676
LENGTH: 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 60/234,687 FILING DATE: 2000-09-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: PCT/US01/00670 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: PCT/US01/00664 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PCT/US01/00667 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 60/236,359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: GB 24263.6 FILING DATE: 2000-10-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 2000-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: PCT/US01/00661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: PCT/US01/00668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: PCT/US01/00665
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5. US20020048763A1
Similarity
5; Conserv
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Rank, David R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chen, Wensheng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hanzel, David K.
86.1%; S ilarity 100.0%; Conservative 0;
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Score 31; DB
s; Pred. No. 22;
0; Mismatches
                    DB
22;
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0;
                                                   Length 53
  Indels
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Gaps
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61 IFFWYK 66
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; LENGTH: 58
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-867-550-866
                                                                                                       ; TYPE: PRT
; ORGANISM: Homo sapiens or Caenorhabditis elegans
US-09-205-658-325
                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-205-658-325
; Sequence 325, Application US/09205658
; Patent No. US20010029617A1
; GENERAL INFORMATION:
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US-09-867-550-866
                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 325
LENGTH: 79
                                                     Query Match
Best Local
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Topper, James
TITLE OF INVENTION: No. US20020082206Alel Polynucleotides from Atherogenic Cells
TITLE OF INVENTION: Thereby
ETILE REFERENCE: 21402-013 (Cura-277)
                                                                                                                                                                                                                                EARLIER APPLICATION NUMBER: US98/10080 EARLIER FILING DATE: 1998-05-15
                                                                                                                                                                                                                                                                   EARLIER APPLICATION NUMBER: 08/857,076
EARLIER FILING DAYE: 1997-05-15
EARLIER APPLICATION NUMBER: 08/888,534
EARLIER FILING DATE: 1997-07-07
                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/205,658
CURRENT FILING DATE: 1998-12-03
                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Ruvkun, Gary
APPLICANT: 099, Scott
TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
TITLE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE CONDITIONS
FILE REFERENCE: 00786/351004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Thereby FILE REFERENCE: 21402-013 (Cura-313) CURRENT APPLICATION NUMBER: US/09/867,550 CURRENT FILING DATE: 2001-09-20 PRIOR APPLICATION NUMBER: USSN 60/208,427 PRIOR FILING DATE: 2000-05-30
                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS:
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                               Local Similarity
les 5; Conserv
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IFFWIK 6
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Conley, Pamela
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                                     Conservative
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83.3%;
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80.0%;
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Pred. No.
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Pred. No.
                                      Mismatches
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31;
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24;
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Query Match
Best Local Similarity
Watches 5; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Escherichia
US-09-815-242-10465
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SEQ ID NO 10465
LENGTH: 951
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                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
                                                                                                                   APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification
TITLE OF INVENTION: Prokaryotes
                                                                                                                                                                                                                                                            APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari L. APPLICANT: Zyskind, Judith W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
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PRIOR APPLICATION NUMBER: 60/269,308
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PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                    APPLICANT:
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Zyskind, Judith W.
                                                                                                                                                                                                  Carr, Grant J
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Xu, H. Howard
                                                                                                                                                                                 Yamamoto, Robert T.
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                                                                                                                                              of Essential Genes
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. 2.9e+02;
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Query Match
Best Local Similarity
Thehes 5; Conserve
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-291A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Salmonella US-09-815-242-13853
                                                                                                        GENERAL INFORMATION:
APPLICANT: Leach, Martin D.
APPLICANT: Mehraban, Fuad
APPLICANT: Conley, Pamela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6, Application US/09935291A Patent No. US20020107373A1 GENERAL INFORMATION:
                                                                                                                                                                                           Sequence 832, Application US/09867550 Patent No. US20020082206A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              \begin{array}{ll} \text{SOFTWARE: FastSEQ for Windows Version} \\ \text{SEQ ID NO} & 13853 \end{array}
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Best Local Similarity
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APPLICANT: Chun, Miyoung
TITLE OF INVENTION: 49937, 49931, AND 49933, NOVEL HUMAN TRANSPORTER
TITLE OF INVENTION: EAMILY MEMBERS AND USES THEREOF
EILE REFERENCE: MNI-184
EILE REFERENCE: MNI-184
                                                                   APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/250,932
PRIOR FILING DATE: 2000-11-30
NUMBER OF SEQ ID NOS: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/935,291A
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: 60/226,504
PRIOR FILING DATE: 2000-08-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Ver.
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PRIOR FILING DATE: 2000-12-2
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
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APPLICANT: Topper, James
TITLE OF INVENTION: No. US20020082206Alel Polynucleotides from Atherogenic Cells
TITLE OF INVENTION: Thereby
FILE REFERENCE: 21402-013 (Cura-313)
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                                                                                       Law, Debbie
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80.0%;
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    Mismatches

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Pred. No. 3.7e+02;
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. 2.9e+02;
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APPLICANT:

Godowski, Paul J.

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US-09-992-598-177; A
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                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 51
LENGTH: 312
                                                                          GENERAL INFORMATION:
APPLICANT: Ashkenæzi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
                                                                                                                                                                                                                                                                                                                    Best
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SEQ ID NO 832
LENGTH: 137
TYPE: PRT
                                                                                                                                                      Patent No. US20020160384A1
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FEATURE:
OTHER INFORMATION: human GR09
09-393-634-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: SF, a No. US20020051997A1el Family of Taste Receptors FILE REFERENCE: 02307E-098000US CURRENT APPLICATION NUMBER: US/09/393,634 CURRENT FILING DATE: 1999-09-10 NUMBER OF SEO ID NOS: 92
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4; Conserv
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Gerber, Hanspeter
Gerritsen, Mary E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The Regents of the University of California
The Government of the United States of America
as represented by the Secretary of the
Department of Health and Human Services
                                Fong, Sherman
                                            Ferrara, Napoleone
                                                             Eaton, Dan L.
                                                                                                                                                                  Application US/09992598
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PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
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PRIOR APPLICATION NUMBER: 60/062250
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CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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OR APPLICATION NUMBER: 60/066770
OR FILING DATE: 1997-11-24
OR APPLICATION NUMBER: 60/075945
OR FILING DATE: 1998-02-25
OR APPLICATION NUMBER: 60/078910
OR FILING DATE: 1998-03-20
OR APPLICATION NUMBER: 60/083322
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APPLICATION NUMBER: 60/084600
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Kljavin, Ivar J.
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RESULT 11
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APPLICANT: Ashkenazi
APPLICANT: Baker,Ke
APPLICANT: Botstein
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OR APPLICATION NUMBER: 60/091519
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OR FILING DATE: 1998-07-02
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OR APPLICATION NUMBER: 60/090540
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APPLICATION NUMBER: 60/090694
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                                                                                                                              Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Grimaldi, J.Christopher
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Baker, Kevin P.
                                                                           Gurney, Austin L
Kljavin, Ivar J.
                                                                                                                                                                                                                                                                      Fong, Sherman
                                                                                                                                                                                                                                                                                                                             Eaton, Dan L.
Paoni, Nicholas
                                                                                                                                                                                                                                                                                                   Ferrara, Napoleone
                                                                                                                                                                                                                                                                                                                                                          Desnoyers,Luc
                                                                                                                                                                                                                                                                                                                                                                                 Botstein,David
                       Pan, James
                                                 Napier, Mary A.
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TITLE OF INVENTION: Secreted and Transmembran
TITLE OF INVENTION: Acids Encoding the Same
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APPLICATION NUMBER: 60/088742
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                                                                                                                                                                DATE:
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art, Timothy A.
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NUMBER: 60/089952 1998-06-19

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60/090445 60/090444 60/090435 60/090431 60/090429 60/090355 60/090349 60/090254 60/090252 60/090246

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APPLICANT: Eaton, Dan L.
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FILING DATE: 1998-07-07
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APPLICATION NUMBER: 60/091633
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APPLICATION NUMBER: 60/091978
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APPLICATION NUMBER: 60/090696
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PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
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CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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PRIOR APPLICATION NUMBER: 60/075945
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PRIOR FILING DATE: 1997-11-13
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DR APPLICATION NUMBER: 60/087827
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DR APPLICATION NUMBER: 60/088021
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APPLICATION NUMBER: 60/087106
FILING DATE: 1998-05-28
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FILING DATE: 1998-06-02
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Stewart, Timothy A.
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Williams,
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NUMBER: NUMBER: 60/ : 1998-06-04

60/088028 60/088026

PRIOR PRIOR

FILING DATE: 1998-00 APPLICATION NUMBER: FILING DATE: 1998-0 APPLICATION NUMBER:

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60/088655 60/088217

FILING DATE: 1998-06 APPLICATION NUMBER:

1998-06-10

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APPLICATION NUMBER: 60/088742 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/0 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088734 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/0 FILING DATE: 1998-06-09

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APPLICATION NUMBER: 60/ FILING DATE: 1998-06-04

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OR FILING DATE: 1998-06-17

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OR FILING DATE: 1998-06-17

OR APPLICATION NUMBER: 60/089598

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OR APPLICATION NUMBER: 60/089599

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OR APPLICATION NUMBER: 60/091544
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OR FILING DATE: 1998-07-02
OR APPLICATION NUMBER: 60/091633
OR FILING DATE: 1998-07-02
OR FILING DATE: 1998-07-07
OR APPLICATION NUMBER: 60/091978
OR FILING DATE: 1998-07-07
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APPLICATION NUMBER: FILING DATE:

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APPLICATION NUMBER: 60/089907 FILING DATE: 1998-06-18

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FILING DATE: 1998-U5-LU
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NUMBER: 60/089512 1998-06-16

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60/089440

APPLICATE: 1998-00 APPLICATION NUMBER: 60, APPLICATION NUMBER: 60, TWO DATE: 1998-06-1

60/089105 60/088876 60/088863

APPLICATION NUMBER: 60/ FILING DATE: 1998-06-11

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CURRENT FILING DATE: 2001-11-14
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R APPLICATION NUMBER: 60/08
R FILING DATE: 1998-05-28
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R FILING DATE: 1998-06-02
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FILING DATE: 1998-06-04
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FILING DATE: 1998-04-28
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APPLICATION NUMBER: 60/065186
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FILING DATE: 1998-06-04
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Baker, Kevin P.
Botstein, David
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PRIOR DR FILING DATE: 1998-06-19
R APPLICATION NUMBER: 60/05
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RESULT 15
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US-09-989-730-177
Sequence 177, Application US/09989730
Publication No. US20020197674A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi, J.
APPLICANT: Baker, Kevin P.
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Williams, P. Mickey
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Grimaldi, J.Christopher
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